

FIGURE 1

CGGACGCGTGGGTGCGAGGGCGAAGGTGACCGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCA**ATGT**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCAAGGCCCTCCCCGTGTGTGAAGAATTCATCAGCAAGAATCA
 ATGGCTGTTAAACACCTAGCAGGGAAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAATT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAAATGGTGTGACCTTTGACGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCCAAAGCATCTTCTGTTGGTTGCTACATTCGTTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAAATATTAGGGGGTCCCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTTGGGAGGCCCTCTCCACTGTGGCCATGTTGCGCCCAAGTGAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACCGTGGATT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAAGAA**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
 ATTAATAAGTTTGTACAAGCAGCTTTCSTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCTCATGTTTGGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTGTGTATGAGAATGTAAGTCTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAAATTTGTAATTAATGTCAAGTGATTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGCTATTGTTACATTCATTT
 GCTGAACCTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATGCATTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCAATGTTTGAAGTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACATTTCTCAAGAGAAAAATTTCAAGCATGAAATATGTGCTTTTTCAG
 AATACAAACAGTATACATCATG

00000727-11001

GAAGGCTTGCCCTCGCTGTGTCGGAATTCGGTGGCGCCACGTCGCGCCCGCTTCGCCCTTCTGACG
CGCGGCTTTCGGCGGGTTCACCATAGACACCTAACAGTCGCGGAGCGCGGCCGCTGCTGAAGG
GGTGGCGGACGGGGAGTCGGGGGGTCTTGTGCATCTTGGCATCTGTGGGTCTGTTGGGTTCGAAAGATGTCGG
ACATCGGAGGACCTGGTTCAGGAAGCATCCCGCGCATACGCGCTATTGGTCTCGCGGACCGCATGCTC
CCGCTGGCCCTTGTGTCGGCAAACTCGGCCTCATCAGCCGGCCCTATCGGCTCTCTCTGGCCGCA
AGCCCTCTCTTATTCGCTTTCTCAGATTTCGGAGGCGCAACGCTGCTCTTTATTTCCCTGTGG
GTCCAGGAAGCTGGAATTTCTTTATTTGGTCAAATTTTATATCATGATTTCACGCA
CTTTGAACACAGGAGGCTTTTGTATGGGAGGCGACACACTATTTATCATGCCTCTTTAACTG
GATTTGACCTGTGATTACTGGCTTACGAACTGGATATTCAGTTGCTGATGTTCTCTGTATC
TGTCGACTACTTTATGCTCGGGCTTACCTTACCTGGGTTATCTCTGGATTCACTATATCATCGGAG
ACCGATTATTAAGGCTTTTGGAAATCTGGTTGGACATCTTTATTTTCTTAATGTTTGA
CTCGGTAAATTAAGAGCTTTTGGAAATCTTTTATTCACCAACTCAGTTTGTGATCCCTGG
GATACCCATTAAGAGGAGGAGTATCAGGATTGGTGTCGCCCTCTAGCATAGGCGGAGC
TGCTGATCAGAATTGGCGGAGCGGGAGACCAACTGGGCGCGGGCTTTCAGTTTGGAGAC
AGTGAAGGCGCGCTCTCGGCGACGCTCTCTCAAGCCACATTTCTCCAGTGCCTGGGTG
CACTTTAACAACTCGCTTCTGGCTAACACTTGGACCTGACCCACACTGAATGTAGTCTTTC
AGTACGAGCAAAAGTTCTTAATCCGAAAGAAAATAAGTGTCCAAAGTTTTCAGAT
TCTCATCTCAAGTCTTACTGCTGTGAAGAACAAATAACCACTGTGCAAAATTGCAAAAGCTGAC
TACATTTTTTGGTGCTTCTCTCTCTCCCTTTTCGCTGTGAATATGGGTTTTAGCGGGTCTT
AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAGGACCTTATCTCTT
TCTTGTCAGCTGACTGCTCTCTCCACTTTTCCCAACCCCACTTTTGAACATGAAAAGATTG
CCCCATAAAATGCTCTGCCCTGACAGGTTCTGTATTTATTGACTTTTGGCAAGGCTGGTC
ACAAACATCATATTTCAGTTATTTTCCCTTTTGGTGGCAAGCTGTACCAATAGGGGGAG
AAGACGCGCCAGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
AACCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAGTACCACTGAGTTCATGAGGGCCA
CAGATTGGTTATGAATGATAGATCAGAGGTTGGTGCTGGGTGTTTGTGTTCTGAGCTAAGTGA
TCAAGACTGTAGTGAAGTTGCAGTAACTGAGGTTAGGTTTAAACACTGGGGGATGCACCC
TTTGCTTTTCAATGTATGTCCTTCTGCTTGTGTAGCTGGAGTATTTGGGTGCTTTGTGT
TAGGAGGATCCAGATCATGTGGTGGCTACAGGAGATGCTCTTTTGGAGGTTCTGGGCATTG
ATTCCTCATTTCAATCTCATCTTGGAATGTGTGTCATTGATTAAGGAGGAGAGACCCCTAT
CGCTATTTAAATGTCACTTTTGGCCTATCCCGGCTTTTGGTCATGTTTCAATTAATCT
GAGGAAAGGCGAGCTCTCTCTGCGAGTGATCATTTTAAAGTTTAAAGTTTCTGCTCA
AGGAAAGGCACATGAATTAAGGTTGAATGGCTTTAGAATCATTAAGGTTTGGGCTTGGT
TTTTAGTCTGATGAATGTACAAGCTCTGTGAATAGGACCACTTAAGAACCCACCTTTTT
TCGTAGGTGGGGCTTTCTCATCAGAGCTGCTGCTGATCTGAAGACAGTCTTTTGAAGGCCA
TGCGCTTTACACAGCTTTTGTGGCACTTGAAGTCTGAAGACAGTCTTTAGGAGAGT
ATTGAGTGGCTGTCACTGTTGGTGGCACTAAAAGGCTTCAACAGTTTGTAGTCAGTTCTT
TTCAGGAACAAGCTGCTAGTGAAGTACAGTATGACTATCTTCTCCCGACTCTAAACAGTGTGAT
GTGCTCTTCAATTAATTTATATGATAAAATGAGTGGGAGAGTGTGAACCTTAAGTCTCA
GTTTTGTTGTTCTATCTGTGCCACAATAAAGTTTACTGTAAATTTTAGAGGCTACTTACT
GCAATATGTTGTCAGCTACACTATTGTACAGGCTGGAGACTATTGATATGATAAGAATA
TCTTCGACAGTGAGTGAACCGGAGTCTGTGTTACCCCTTTCACGTCAGGCTGCTCGGAG
CAGTCACTTTTTCTAAAGGTTTACAAGTTTAGAAGCTTTTCACTTCAGGCGAAATGTTCT
ATGAAGTTTATCTCTTAAACATGGTTGAGAGCTGTAGTACGTTATGATATTTGCTGGATT
ATGTTTCTGAATAATTTTACCAAACAAGCTATTGATGTTTGACTTGACAAAGGCAAAACA
TGACAGTGGATTCTCTTCAAAATGGAAGAAAAAAATCCTTATTTGTATAAAGGACTCCC
TTTTTGTAACTAATCCTTTTTTATGTGAATAAAATGTAATATAAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLEFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGFRLL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCCGCGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTGGCC
 CCTTTGGGGCGGGATGGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCACTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAAGAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCTCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTATAAGTA
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEVWVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEESKLTYYTEIHQEYKELVEKLEGLYKEIGINEDQFQEAactsPLAKHTTSQAILQP
VLAEDFTIFKAMMVQKNIEMLQAIRIIQERNGLVPDCLTDGSDVVSdleHEEMKILREVL
RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPENTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGC AACCTGTGTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGGCTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAGAAAC
 AGTGGAAATGGAAACAGTGCCTGTAGTCATCTGTAATATGCTCCTGTGCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCCGTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTCGCT
 TTTCTTTATTTCTGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACAGGCATG
 GCTGTTATCTTCTCAAATTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGTGAA
 GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATATAGTCCAGTGTTTTATTTCTTCAATGGCT
 AATATCTATAAAGTAAGTACTGAAGGAGGGGAACAGCTCAGTGAAGAGATCTTCATACA
 GAACAGCAAAGTCAATTTCTTTGGCATCTGTTTAAATGGGCTGACTCTGGGCTTCAGAGGA
 GTAACCGTGAATCAGATTAAGAAGTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAAGTGCATTTCCAGGGCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTTGTATGGCCAGGTACCACTGTCAATATACAACAGTGTCTGCTCCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAACCCCAAGAGTGATGAGTCAGATGAAGATACTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTTATTTTACATTTTCAGTGTGTTGTAATATTTACTTTTCACTTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCAAAGAACTGATACAGGAGTAACA
 ATATGAAGAAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCGAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGTGTGTAATAATCATGTTAGCTATAGTGTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 TCTCCCTTTTAAACATATAAAAGCTAGGTTGTCTTCTGAAATTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAGAGGACACGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTGCTAAATATTTTCTGTAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTAAAAATTCATGGGAAATTTGGATTTTTGT
 AATAATCTTTTGTATGTTTTAAACATTGGTTCCTAGTCCACATAGTTACCAGTGTATTTTTA
 AGTCAATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAAATATTACATTTTGGAGAATAAGAGGGCAATTTTATTTTATTAGTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAGAACTATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGATGAATATTAACTCTAAAAATGAAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATGGATTTTCTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAAGGTGATAGATGATATTAA
 AAATTAGCAAAACAAAGTGAAGTGTCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGCGAGGCTGTATGTTTACAGACTACCATCTGTAATATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACATTATATAAATTCATTGTGATATCCACAATAATAGACTGGCAGAAGTTG
 GTGGAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPNSNCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGCTGAAGAGGCGTCTAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTTGTGCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGCGCGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTCGCGGGCAGAGGAGCAT
 CCCGTCTACAGGTCCTCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGCGCGCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCACAAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAAGTGACGGGCTGTGCCTGGGTTTCTTCTTCAGATCTAC
 CTATTG**ATG**TGGCTCAGGTGGGCCCCCTTCTCTGCCTCCATCATCCTGTTTTGTGGGCCGAGC
 CTGGGATGCCATCAGACACCCCTTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTTGGCCGTATTGCCTACTTCCCTC
 ATCTGGTTCGTGCCCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTACTCTGATCTGGGCGTGGCGGAGCAGAGAAACCTATGAAGCCACGACAGCTG
 AGCCAATCGCCTACTTCCGGGCGCTACGGCTGGTTCATGAGCCACGGCCATACATCAAACCTT
 ATTACTGGCTTCTCTTCACTGCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCCTTCCAT
 GGAACCGAGCCCATCTTCTCTCCTTCTATGCTCTTTCACCAAGTTTGCCTCTGGAGTGTC
 ACTGGGCATTTTACCTCTAGTCTGGACTTTGCAAGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGAGAAAGAA
 GGCCCTGACGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCT**TAG**GGCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCACAGGACACTTGCTGTGCTCATGTGGGGCCGGCTGCTCTG
 TGGCCTCTGCTCTCCCTCTGCTTGCCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTCATACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYFIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTCAGGT
ATGAGCAGGCTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATG
GGTGGTTTCAGCAAGGCTCAGTTTCCTTCCTTCAGCCCTTGTAAATTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
ACTTCTATTGTGGCAAACCTCCAGAAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATATATATGTTTGTTCAGACCATCCTTCCTACCAATG
CAGCCCAAAATCCATGGCAACAAGTCTTCTGGATCAGACTGTGTGTTGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTCAGAAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGATTTGGGAAAGGTTACAGAAGTTGCTTA
TCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTATCTCAGAAAAATAAGTCAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI¹FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTI²LSYQM³QPKIHGKQVFWIRLLLV⁴WCGVSALSMLT⁵CSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT⁶YIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
219

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTTGAAGCAGT
TACCAAGAATCTTCAACCCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC



FIGURE 17

CCCACGCGTCCGCCGCCGCTGCGTCCCGGAGTGAAGTGAGCTTCTCGGCTGCCCCGCGG
 CCGGGGTGCGGAGCCGAC**ATG**CGCCGCTTCTCGGCCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGTGCTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAAGTGGTTCTTGAACCTCTCGGCCCCAATTCGAACATT
 CCCATCGTGCAAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCCTATTAATAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACA**TGAT**CTGGATTTTCTGTTTGCCACATCCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCCTCTAAAGCCCCCTATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATT
 ACAAGGTGAGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLFLFCGAYLYKQGFaipGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPFDKVALLRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGGGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTTGTAGTCAATCATTTT
 CCAGTTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAA
 TAGGAAAAATAACTTTGGGATTTTATATTGGAAGAC **ATGG**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTGGTGAGACAGACCGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAAGATGAACCTCAGAGACC
 CCCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTAGCCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCATTGCCAA
 GAAGTACATGTCAGAAAAAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCTTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAGCCCTGTTGGAGGAAGAGATTCT
 AGCATTTTTTTGTGCCAGTACCCTGAGGCGACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCTATTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCTGTTTTCACTCACCTGCCATTTCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCACTCTGCGAT
 GGAACCGCTTTCTCAGAACTG **TAG**GAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAAA

MDLAANEISIDKLSETVDLVRQTHQCQMGSEKATEKFIQRLLEKNEPQRPPFPQYPLLIIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLLHHIRLMSLP IAKKYMSENKGVP L
HGGDEDRPFFDFDPWWTNDCEQNESEFIPANCTGCAQKHLKVM LLEDAPRKFERLHPLVIKT
GKPLLEEEIQHF LQCYPEATEPGVSEGF FAKWRCFERPWFPPYPWRRLNRSQMLRELFPV
FTHLPFKDASLNKCSFLHPEPVGSGMKHMDPLFIISGEAMLQ LIPFPQCRRHQCSVAMP
IEPGDIGYDTHHWKVIARCGVQPLVICDTGTFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CACGGTCCCCACTTGCAGCTGCGAGCAGCTGAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
 CCAGTGGTGGCAGCGTCTGATGACCGTGCCCTATGAGCCGCTGGGGCTGACAGTGGGACTGCC
 CTCCTCGCCACCCCAACTATGCGAGCCCACTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGGCCACTATCGACAAACAGGTACAGCCAACTGTCGCGAGTTGCGAATG
 GACACGATGCTTAAGAGCCACGACCTTATGTCAAGTTTCTGGAATGCTCTGATGACATGCT
 TATGACGATGGGACGCGGCCAGTGGGAGCGCGCCAGATCGTCGGGCTTCCAGGAGC
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGGCTACACGGCAGTGCTG
 AAGCAGCGGCAACGACGACTCCATGGCCCTGCTGCATGGGGGGCGCTGTGGCGCCAGCT
 CGCGAGCCCATTTGGGGCTTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 CGCGCAGACATATTTACGCTATGCTGTGAAGCTGGTGCCCAACCATCACTTCGACCCCTAC
 CTGGAAGCGAGCGCTCTCCGAGACAATCTGGGTGAGGTCCCCTGACACCCACCGAGGAGGC
 CTCACCTGCTCTGGCAGTGACCAAGAGGCGAAAGTGAGCACCCACCCGAGTTGGTGAGG
 AGGACCACTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGACGAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACCGTAGTGGCCGT
 GGTCCGAGGGCTGCTGGAGGTACACACAGAATGTATATACTTACAGTGGCAGCACTGAGC
 CGGTGGAAACCGAGGAGGGCATCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGGAG
 GTCCACCTTGGCGGCTTTCAACCTGCGCGGTTGAGCACTTGAGCTCTTCTTATCGATCAGGC
 CACTACTTCTTCAACTTCCCATCAAGGTGGGCGAGCACCCAGTCTCATCTCTTAGCCAGA
 CTCGAGAGCCCGAGCTGGGCCCCATCCACCCCATACCCAGGTACGGAAACCGAGTGTATCTG
 TGGCTCTTGGCGCTACGGCGCCCTCTCAAGGCTACTTAAGCAGCGCTGCCCGAGGAGAT
 GCTCGGTGCTCAGGCCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTCGAGTACT
 TGATCAACTCAACACCATTTGCGGGGCGGACCTACATGACCTCTCTGAGTACCTGTGTTC
 CCCTGGGTCTCTGAGGACTACGTGTCCCAACCCCTGGACCTCAGCAACCCAGCCGTCTTCCG
 GGACTGCTTAAGCCATCGGTGTGGTGAACCCCAAGCTGCGGAGGCTGCTGAGGAGGAGAT
 ATGAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCACATATGGCACCCTACCTCC
 AATGCGAGCGTGATGACCTACCTCATCCGCGTGAGGAGCTCATCCCGAATCTTCTACTTTTCT
 GACTCTCTGGAGAACAGAACCGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTCTAGACCTGGACCATGTGACAGATGAGCGGGAACGGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCACTTCCCTGTCACTGCTGAAGGAGCCACATCAACCTGGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGACAGCCTGGACACTAACTCACCTAGCATCTTCCAGCA
 CCTGGACGAACCTCAAGGCATTCTTCGAGAGGTGACTGTGAGTGCCAGTGGGCTCTGGGCA
 CCCACAGCTGGTGTGCCCTATGACCGCAACATAAGCAACTACTTCAAGCTTCAGCAAGAGCCCC
 ACCATGGGCGAGCCACAAGACGACGCACTGCTGAGTGGCCCGTGGGTGCCAGGCGAGTGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGCTGCGGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCGAGCTGACGCTGCCAC
 CTGTGATGATTAACCTGGCTTGCACCTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCC
 GGACACCAAGCTGTGATGCTGTGGCGGCTCTGATCAGGGTGGTCTGATCAGGCTGGCAGT
 CAAAGCCTGTGAGGCTGTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACTTGACATGGCTGTGTGGATCTGAGGATGGAACGTGATCATACACTGTACGCCG
 CGGACAGTTTGTAGCGGCACCTACGGCCTCTGGGTGCCACATTCCTGTGACCTATTTTCCACC
 TGGCATTTGGGGTCCGAAGGCCAGATTGGGTACAGAGCTCAGGCTGAGGACGCTCTGGGGCC
 CAGGTCACCTACTCCTTGCACCTGTATTCACTCAATGGGAAGTTGGCGGGCTTCACTGCCCC
 GGCAGACAGCCTACAGCCTGACGGTGACAGAGGACTTGTGTTGCTGGGCACCGCCAGT
 GCGCGCTGCACATCTTCAACTAAACACACTGCTCCCGCGCGCGCTCTCTTGGCCATGAAG
 GTGGCCATCCGAGAGCTGACCAAGGAGCGAGCAGCTGCTGGTGGGCGCTGGAGGA
 TGGCAAGCTCATCTGCTGGTGTGCGGGGGCAGCCCTCTGAGGTGCGCAGCAGCAGTTCGCGC
 GGAAGCTCTGGCGGTCTCTCGCGGCGCATCTCCAGGTGTCTCGGGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCTGCAACTGGCCAGTCCGCGTCTCGGGCGCGCCCGCCCGGAGGCGCTG
 CGCCGGGAGGCCCGCCGCAAGTCCGGCGGGAACCTCCGGGGTGGCGAGCCAGGGGGTGA
 CGGGGGCCCACTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGAGTTGGCG
 GCGGAAGTCCCGCCCTCGCGGCTGAGGGGCGCGCTGAGGCGCAGCACTGGCGGTCT

00360721.1.1.001

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRARLEGL
 RYTAVLKQATQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDLNLEGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLEVTQNVFYFDGSTERVETEEGIGYDFRRP
 LAQLREVHLRFRNLRRSALELFFIDQANYFLNFPCKVGTTPVSSSPQTPRPQPQGPPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSPKIGVVPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDNPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGFWVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISSGRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATGGGGTCTTGGGGCTCTTC
 TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCGTCTTGACAAAGTCACAGA
 CCTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGCCATATGTATCGCCAGCGGGCTTCTTACGCGT
 TTTGCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAACAGCTCCGGCCCTGATCCAGGACTGC
 ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCGAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACCTCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTAAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLQIYGVLG
LFWTLNWWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAK
NAFMLLMRNIVRVVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

0
0
0
0
0
4
U
A
A
A
A
0
0
A

FIGURE 26

GAGTCTTGACCGCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGCGT
 GGCT**ATG**TTCGTGTCGATTTCGCAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACCTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
 CAGTGTGACCAAGTGCATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCGACG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCGAGCTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAATCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCCTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACCTGTCTCA
 AGTCTTTGTGTGTTGCAAAAGAACCAGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCAATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGCT**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQPHYFILINCGANVDLLDILQPEDDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAVEDIFRDEEEDEEHSGNDSDGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMD ISKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQT IASCL
CTNLVISQGPFYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAAGAGTTTC
ATTATTTTATTCTCATAAAGTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAAGCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

[illegible]

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCGCAGTTGCTTCGGGACCCAGGAACCCCTCGGGCCGACGCCGCCAGGAAAGACTG
 AGGCCCGCGCCCTGCCCCCGGGCTCCCTGCGCGCCGCCCGCTCCGGGACAGAAAGTGTG
 CTCAGGGTCCCTTCTGCTGCTCGCGTGTCTCTGCTACTGTCGGCCCTGGGGTCTGGGTGACG
 GCTGCCCATTCCGGTGTCCAGTGCAGCCAGCCACAGACAGTCTTCTGCATCGCCCGCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACCGTGGGGCTGTACGTTCTTTGAGAACGGCAT
 CACCATGTCTGCAGCAGCAGCAGCTTTGCCGGCTTCGGGGCTGCAGCTCCTGGACTGTCTAC
 AGAACAGATGCCAGCCTGCCACGGGGGTCTTCAGCACCACCTCCGCAACCTCAGCAACCTG
 GACCTTACGGCCAAACAGGCTGCATGAATACCAATAGACCTTCCGTGGCTCGCGCGCTCG
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCGACCTGGTGCTTCGACACCG
 TCGACCGCTCTCTGGAGCTCAAGCTCAGGCAGACACAGCTCGGGCACTGCCCCGCTGCGC
 TCGCCCGCTGCTGCTGCTGACCTCAGCCACAACAGCCTCTGGCCCTGGAGCCGGCAT
 CCTGAGACATGCCAACAGCTGGAGGCGCTCGGCCTGGCTGTGCTGGGGCTGCAGCAGCTGGAC
 AGGGGCTCTTACGCCGTTTGCACAACCTCAGCACCTGGATGTGTGCGACAACAGCTGGAG
 CGAGTGCACCTGTGATCCGAGGCTTCGGGGCTGCAGCGCTCGGCTGCGCGCAACAC
 CTGACATTCGCCAGCTCGGCCCGAGACCTGCGCGGCTGGCTGTGCTTCGAGGAGAGTGGATG
 TCGCAACCTTAAGCTCGAGGCCCTGCTGCGACATCTCGGGCTCTTCCGCCCTCGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCTG
 GTGCGCGAGAGCCAGCTCACACTGCCCCAGCTCTGAGGAGAGCGCTGCCACTTCCGCCCA
 AGAAGCTGCGCGGCTGCTCTTGGAGCTTACTACGCGACTTTGGCTGCCAGCACCAC
 ACCACAGCCACAGCTGCCCAACACAGGCGCTGGTGTGCGGGAGGCCACAGCTTGTCTTCTAG
 CTGGCTCTACTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCGCCCTCCA
 CTGCCCAACCGACTGTAGGGCTGTCCCCAGCCCCAGACTGCCACCGTCCACTGCTCT
 AATGGGGGACATGCCACTGGGACAGGCGACCCACTGGCTGTGCTTGTGCCCGAAGGCT
 CACGGGCTGTACTGTAGAGCCAGATGCGGACAGGGGACAGGCCACGCCCTACACCACTCA
 CGCCAGGGCCACACGTTCTCTGACCTGGGCATCGAGCCGGTGAGCCCCACTCTCTCGCG
 GTGGGGTGCAGCGCTACTCCAGGGGAGCTCCGTGCGAGCTCAGGAGCCCTCGCTCACTA
 TCGCAACCTATCGGGCTGTATAAGCGCTGTGTAGCTGTCGACTGCTGCTGCTGCTGCTG
 AGTACACGCTCACCAGCTCGGCCCAACGCCACTTACTCTGCTGTGTCTATGCTTTGGGG
 CCGGCGGGTGGCGGAGGGCGAGGAGCTGCGGGAGGGCCATACACCCACGGCTCA
 CTCCAACCACGCCCCAGTCAACCAGGCCCGCGAGGGCAACCTGCCGCTCTCATTGCGCCG
 CCTTGGCCGCGTGTCTCTTGGCCGCGCTGCTCGGTTGGGGGACGCTACTGTGTGCGGGG
 GGGCTGCAGTGCAGCAGCGCTCAGGACAAGGGCAGGTGGGGCAGGGCTGGGCCCT
 GGAATCGGAGGAGTGAAGGTCCTTGTGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCTCGCCACGCGGTTGAGTGTGAGTGTGCCACTTGGGCTTCCAGGGCTGGCTCT
 CAGTCACCCCTCCACGCAAGCCCTACATCTAAAGCCAGAGAGACAGCAGCTGGGGCCG
 GGCTCTCAGCAGCTGAGATGGCCAGGCCCTCTGCTGCTGCCACACAGCTAAGTTCTCATGTC
 CAACCTCGGGATGTGTGACAGAGGCTGTGTGACACAGCTTGGGCTGTTCCTCTGGA
 CCTCGGCTCTCTATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAAGCTGCAGTCCCTGGGACCGCG
 GGCCCTGCATGTGTGCTGTAAGCATGCTGGGTCTGCTGGCTTCCCACTCAGGGGGA
 CCTTGGGGCGCAGTGAAGGAAGCTCCCGGAAGAAGACAGAGGAGAGCGGGTAGGCGGCTGTG
 TGACTTATGTTTGGCCCCAGGAGCGAAGGAACAAAGAACTGGAAGGAATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCAATTATCTG
 GGAAGATGTTTTTCAAACCTCAGAGCAAGGACTTGTGGTTTTGTTAAGACAACAGTATATG
 AAGGCTTTTGTAAAGAAAAATAAAGATGAAGTGTGA

MCSRVP LLLPL LLL LALGPGVQGCPSGQCQSQPQTVFCTARQGTTVPRDVPPD TVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRI RHIQPAGFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVBARLRLAGLGLQQLDEGLFSRLRNHLDDLDSVDNQLERVPPVIRGLRGLTRRLRAG
NTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCLPSWFG
FWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCEPE
GFTGLYCESQMGQGRPSPTPTVTRPPRSLTLGIEPVSPSTSLRVGLQRYLQGS SVQLRSLRL
TYRNLSPDKRLVTLRLPASLAEYTVTQLRPNTASVCMPLGGRVPEEGEEACGEAHTPPA
VHNSHGAPDQVQAREGNLPLLIAPALAAVLLAATAVGAACVVRGRGMAAAQKQGVPGAG
PLELEGVKVPLEPGPKATTEGGELPSGSECEVPLMGFFPGGLOSLPHAKPYI

[illegible]

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKT FEFNKELRYLDLSNNRLKSVTWYLLAGLRYL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLQHKNDENC SWPETVVMNLSYNKLS
DSVFRCLPKSIQILDLNNNIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSI SENI
VSFIEKSYKSIFVLSFNFVQNEWCHYEFYFAHHNLFHENS DHIIILILEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCKGLEFWANLRAAINNVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTGCGCGGAAAAGG
 GAGGGAGAAAGGAAGGGCGGGGCGGCCCTCTGCGCCCGCCCGCGCTCTGCGCGCCCTGTCTGCGCCCGGCG
 CCAGCCCGACCGCCGCGGGGCGGTACACGCGCAGCCAGCGCGCCCTCTCGCGCCCAAGCGCGCCCT
 CTGCTGTGCCCTGCGCCCTTGCCTCGCGCCGAGCTTCTGCGCGCAGCCCGCCCGCGCGCCCGGTGACGCTGA
 CCTCTGCTTGGCGCGGGGCGGACGAGC**ATGT**CCCGCCGGGACCCGTACCCAGCGCTGCCCTTGGCTGCTC
 CTGGCAGTGACCTTGGCGGGGTGCGAGCCCGAGGCGCAGCCCTCGAGGACCCCTGATTATTACGGGCAGGAGAT
 CTGAGGCGGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCTGCTGCGGGG
 CCGGGGAGGAGTGGGAGCGGCGCCCGCAGGAGCCCGAGGCGCCCAAGCGCCCAAGAAAGCTGCC
 AAGAGGGGAGAGTGGGCTCGGAGCCGCTCCACAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG
 CTCTGAGAAAGGTGCCAACGATGATCACAGTGTCCGTGTGGCCGTGAAGATGTCAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGCATTAAATGAAATGATTTTATGACGGAGCGTGGTGGCGGGGAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACAGATTCACTGGTGTATCACTCAAGGGA
 GGAACCTCCCTTGGCTGAGTGA CTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACACGTGGGT
 ACTGTTAAGAATGGATCTGGAGACATGATATTGAGGGAACACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGGTGGCCCGCTACATCCGCATAAAACCTCAGTCTGGTTGATAATGGGAGCATCTGCATGA
 GAATGGAGATCTCGGCTGCCACTGCCAGTCCGAGTCTTAATAATTATATCACCGCCGGAAGCAGATGACCAACCT
 GATGACCTGGATTTTAAGCACCAAAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTAATGAAATGTGTCC
 CAATATCACAGAAATTTACAACATTTGAAAAAGCCACCGGGGCTGAAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGGAGCATGAAGTGGCTGAGCCGAGTTCCACTACATCGCGGGGGCCACCGCAATGAGGTGCTGGGCG
 CGGAGCTGCTGCTGCTGCTGGTGAGTTCTGTGTGTCAGGAGTACTGGCCCGGAATGCGCGCATCGTCCACCT
 GGTGAGAGAGCGCGGATTACAGCTCTCCCTCCCTCAACCCCGATGGCTACGAGAAAGCTCAGAAAGGGGCT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGAACCCAGATGGAATGACATCAACAACAACTTCTCTGATTTA
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAAATGTCCCGAGGAAAGTTCCCAATCACTATATTGCAATCCC
 TGAGTGGTTTCTGCGGAAATGCCACGGTGGCTGCCGAGACCAGAGCAGTCAATGCCCTGGATGGAATAATCC
 CTITTTGTGCTGGGCGCAACCTGCGAGGCGCGGAGCTGGTGGTGGCGTATCCCTAGCAGCTGGTGGCGTCCCC
 TGGAGAGCGCAGGAACACACCCCGACCCCGATGACACAGTGTTCGCTGGCTGGGCTACTCTTATGCTCCAC
 ACACGCCCTCATGACAGCGCCCGGAGGAGGTGTGCCACACGGAGGACTTCCAGAGAGGAGGAGGCACTGCA
 ATGGGGCTCTCGGCACACCGTCTGCTGGAAGTCTGAACGATTTCACTACCTTCATACAACTGCTTCGAATCTG
 TCCATCTACGTGGGCTGTGATTAATACCCACATGAGAGCCAGCTGCCGAGAGGTGGGGAATAAACCGGAACTC
 TCTGATCGTGTTCATGGCAGAGGTTCTCGTGGCATTAAGGCTTGGTGAGAGATTCACTGGAAGAAGAAATCC
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACATGACATCCGAACAGCACAAGTGGGGATTACTGGCCCTC
 CTGAACCCCTGGAAGATGATGTGCTCAGAGAAAGCCGCAAGGTTTCACTGCATCCACCAAGAATGTATGGTTGG
 CTATGCTAGTAGGGGCAAGAAGTGTGACTTCACTTAGCAAAACCAACATGCCAGAGTCCGAGAGTCAATGG
 AGAAGTTTGGGAGAGCCGCTGAGCTGCCAGCCAGGCGGCTGAAGCTGCGGGGCGGAGAGACGACGAGCT
 GGGTGA**CA**CCCTCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAATTAACCAACCGCTGGTAGTAGCTCCATAG
 TGAAGTCACTCACTGTTGTTCTCTGTAATTCAGAAAGTGGCTGGAAGAGAGGGTGCAATGTGGAGCGAGTCC
 CAAAGGGGAGAGCTGGAGGCTGAGGCTGTTTCTTTCTTTGTTCCCATTTATCCAAATTACTTGGACAGAGCA
 CGAGAGAAAGCTGATGGGAGTGTGAGAGAACTCAGCAAGCCAACTGCGAGGAGCAGAGAGAGAGAGAGGAGG
 GAGCTGTGCGGTTCAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGTCTCCCTGTTTGGCTGGCAGCAGG
 GTTCCAGCTGGAATTTGCAATTTGACAGCTAAAATTCAGCAATTTCCCGAGCTGGGCTGTGCCAAATGTACCA
 TTGTGAGTGCTCCCGAGGCTCTAAGAGAATCCACCTCTCTGGCCCTGGGACATTTGAAGCTGCTCAATTA
 ATTCTGATTTTTCACAAATAGCTGATTGCCAAGTGACATCGCATGAGGATCTGGAATCTGTTTATCTCTCT
 TTTTCAACAAAGAGTGTTGTCAGAAAAGGAGAGAGAGGCTGAGATCATTCAGAGATTGTTGGGCAAGAGCA
 TGGAGCTTCTTTCACAAATTTCTGGTCCATAAAACCCCAAGTCCCTGCTGATGAGAGCTTATGAAATTA
 CCCCAGTGTAGGAGAGCCAGAGGTCGCCACCTTCTGAAGGGCCAGAAATTTAGCTTGGATCTCTCTCTTTATC
 CTGCTAGGACTGGAAGAGCCAGAAAGTGGGTGGCTGAGCCCTGCTCTGCTGAGGATTGGCCCTGGAGTG
 GAAATGAGTGCTCATGGGTTGGCTCATATCAGCTGGGAGTATTTTGTATATGAGAAGTGCAGATCTCCA
 GATTAGCTGAAATGTAATGAAACCTCTTAGGATTTATCTGTGGAGCATGATTTGGAAGAATATTGAATTA
 CTTCAGAGAAAAAGTATGCTCACTTTTGTAAATGTTGCTGCCTATTGACCTGGGAAAAATGAAAAAAA
 AATAAAGCAAAATGGTAGACCTTTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEFELETFSPPPLP
AGPGEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVS LPARR
LKLRGRKRRQRG

FIGURE 37

CTAAGAGGCAACATGAGGCCGGCCTCTCATTCTCTAGCCCTTCTGTCTCTTCTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCACAGCCCGGCTTCAGCTCTTTCCAGGTGTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGAGCTTAGCGAGCGGAGTTCTGTGCTCCAGTTGTT
 TCTCAATTTACCGGCTCCGTGGATGACCTGGGACCTGCCAGTGTCTGTCTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGAGTGGAAAGCTTGGAAATCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATTAGTGTATGAAGAAGAACTGTTAAACCTTAACCTGCCAATTGACATCAT
 GGAGAGGATACCAATTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGAAAAAT
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTGACCACTGGAGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCTTGCCATTTCGCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCCCTTAAAGATCAAAACACCCCTGTGCTCCACCCTCTCCCACTC
 CAGGGAGCTGTGGTCATGTTGGTGTGGTGAACATCAGCAACCCGTCTGTGGTTGAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTCTTGGGGTAGGGATTACTCTCCCAAGCATCCAAACAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACAACGGGAATATTGCCAGAGTTAACTGACCACCAACAGGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTTATTCACTGAAGCCAGCACTGGTAACATGGTATAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCGCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGACTATGAACACCAGAACAGAGAGATTTTTACTATTATGACACAACACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACAGAAA
 CTTTATGTCTATAACGATGTTTACCTCTGAATTATGATCTTCTGTCTTGCAGAGGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAAGTGTGTTTCAATTTGACGCAATGTTAGGTGCATAGTTCTACCACTAGAGACTAGGACATTTGTCT
 TGATTGTGTAGTTCTCTTGGGAATCATCTGCCCTTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAATATA
 GGAATTAAGGAACCTAAAACTCAGTATGGCGCTAGGGATTCTTTGTACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCATAATCTTCCATGCCTGGAAGAAACCTGGGCACTTAGTTAGGTAGATTAAATATCT
 GGAAGCTCTCGAGGGACCAAATCTCCAACTTTTTTCCCTCAGTACGCACTGGAAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATCTACATCTGTAAAGTGTGAGTTTATGGAGAGAGGCCCTTTT
 ATGCATTAATTTGATCATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACTGCTTTTCTTTCTCTC
 ATTGCTCCACTTACTAAAAGTCAGTAGAATCTTCACTCATAACTTCCCTCCAAGGCGAGCTCAGAGAATTAG
 AACCACTACTAAACAATTCCACCCCCACCAACCCCTTCTACTGCCTACTTAAAAAATTAATAGTTT
 CTATGGAATGATCTAAGATTAGAAAAATTAATTTCTTAAATTTCTATTTAGGACTTTTATTTACATGACTCTA
 AGACTATAAGAAAACTGATGGCAGTGACAAGTGTGACATTTATTGTTCTATAAAGACCTGGAGCATATA
 TGTGCACTTATGAGTGTATCAGTTGTGCAATGTAATTTTGCTTTGTTTAAAGCTGCACTGTGAAGAAAT
 GAAAAATTAATTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCACTGAGCTAGT
 TGAACCTCTGCGGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTATCATCTAGTCTTTGTCTATTTT
 TCTTTGATGTCTAGTCTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTAAAAATAATGAT
 TAAAAATGTCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

MRPGLSFLALLFFLGLQAAGDLGDVGPPIPSPGFSSFPFVDDSSSSFSSSSRSGSSSSRSLGS
GGSVSQLFNFTGSGVDDRGTCQCSVSLPDTTFPVRVERLEFTHAVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKEFSGGSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQPHPNKGLYWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYGQSGGTAVYNNMYNMVNTGNIARVNLTTNTIAVTQTLPAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCVGLYATRMTNRTBEEIFYDDTNTGKEGKLDIVMHMKQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSLQTKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGGGGAGCGTCCTGGGGGCTGTGCTCCATGGCGAGCT
 GGAATACCATTCTTGTGTGGAAGTGCCTCGTGTTCGTATGCCATGCTGCTCATGTGGAATC
 AACTCCCATCTTAACTAGATTGATCTATGCACTTTTCTTGGCTTTGGAGATATGTGTAGCTTG
 TGTAAATTTGATACCAAGGAATGGAAGAACAACCTGAATAAGATTCTCGGATTTGTGAGAAATG
 AGAAAGGTTGTCTCCCTGTGAACATTTTGGTTGGCTATAAAGCTGTATATCCTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTTCTCTTCTTACTAATGATCAAAAGTGAAGACGTAGCATGA
 TCCTAGAGCTCGAGTGCACAAATGGATTTTGGTTCTTTAAATTTGGCTGCAGCAATTCGAATTA
 TTATTGGGGCATTTCTTCATTCAGAAGGAACTTTACAACCTGTGTGGTTTATGTAGGCATG
 GCAGGTGCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCATTTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCAATCCAGCCAGTTGTTCCAGAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAGAATACACAACAGATCTGGTT
 TGTACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCCAGAAACAAATTCGAACCCAAAGTCTACTAAGCATTAATTGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGGTGGCATGCTCAAGGAATATAGGACTAATTC
 TCTTTTGTGTGTGTATTTTATCCAGCATCCGTAACCTCAAAACAATAGTCAGGTTAATAAAA
 CTGACTCTAACAAAGTATGAATCTACATTAATAGAAGTGGTGGAGCTAGAAGTGTAGGATC
 ACTGGAGGATGGGGCAGTGTCTCACCAGCTGTAGATAATGAAGGGATGGTGTCACTTACA
 GTTATTCCTTCTTTCATCATGCTTTTCCCTGGCTTCACTTTATATCATGATGACCTTATCC
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTATGTTTGGACACTCGTGGCACCCTTGTCT
 TTAACAATCCGTGATTTGACCTGAGACTTCTAGCATGAAAGTCCCACTTGTATTATTTGCT
 TTATTTGAAACAGTATTCCTCACTTTTGTAAAGTTGTGTATGTTTGTCTTCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTGTCTATTTTGTATTTTCTTACCAA
 GTGCATTGATATGCTGAAGTACAATGAATTGCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAAAGTGCCATTATTTGGGCTTATTTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAATGTTTGTGACTATTTTAAAAATTATATAGACCTTAAGCTGTTTGTAGCAAGCTAAAA
 GCAAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATACGCAAGAAAC
 ATGGTTTATTTTAAAAATTATAAACCAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTGTAGTGGCAATAGTGTAGG
 TTAGGGATGGAGTGTGCGTACTAAATTTGAATAACGAGTAAATTAATCTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTGTTTGGTTGTTTTAACTCATGAAGTATGGGTTGAGT
 GGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCCAGCACGGTAGCTCACCTTT
 GGTATCCCAAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCCAAGGAATTCACCA
 GCTTGGCCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCTGTGGTC
 CAGCACTGAGAGCTAGTGAAGATTGCTGAGCCCAAGAGCCAAAGGTTGCACTGAGCAAGTCA
 CGTCACTGCACCTAGCTGGCCACAGAGTAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATGACATTTCTCTGACATTTAA
 AAATAATTTCTATCAAAATACATGCATATTGATTACACCTCATACTGTGATAATTAATGT
 GATGTGGATGCTGGTGTGAGCATGACCCATAAACAGGTGAGAAGATGATGGAATGTTTT
 AGAATAACCTCTGCTTATAGTATACACAGTTCAAAAGATGTTTAAAAATGCTTTTGTAT
 TTACTGCCATGTAAATTTAATGATATAGATTATTTGAACTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTGTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAAAATCTACAATT
 TCTTCTTTAAAAATTTTATTAATGTGAATGGAATATAACAATTCAGCTTAATCCCCAAC
 TTATCTGTGTGTAGACATTTGATTCACAATTTTGAATGGCTGTGTTTTCACTCTAATAATA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTYSSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAAC TTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTTTGNTATGCCGATGCTGTCCAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAAC TGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

AAGAAGCTGTCTCCACTTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATTGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCACCCTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAACAACCT
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCTTGTAAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTGCTTTGGCTATGTTCTCTATCTTCTCTCTTTA
CTAATGATCAAAAGTAGAGAGTAGCAGTGTGCTTAGAGCTGCAGTGCACAATGGATTTGGTT
CTTTAAATTTGCTGCAGCAATTCGAATTATTTATTTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCITGGATTTTTGTGAGAAATGAGAAAGGTGTTGTCCCCCTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCGAGCTCGGTTTGCCCTGCGGATTGAGCTGCGGGTTCGGGCGCGGCGCGGCTCTCCAAT
 TCCAAATGTGTCTGGCTGGAGCGGAGCGCGAGGCTTTCGGCAAAAGGCACTGAGTGTGTTGCGACAGCGGGGCGAG
 TCGCTGGAAGCGAGATAAAAGAAAACATTATTAACGTGCTATTACGAGGGAGCGCGCGCGGCGCTCTCGC
 ACTCCCGCGGGAAGATTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAGAAGCGGAAAGAGCGAGATTAC
 CTGCTTTCCAGCCCAAGTGACCTGATGATGGCCCTCTCGAATTTTATCAGATATTTGATTTATTATGACGATGCC
 CCGTGTGTTGTGTGTACGACACACACGCTGACACAAAGGCTCTGGCTCGCTCCCTCCGCTTTCGAGCTCC
 TGGGCGAATCCACATCTGTTTAACTCTCCGCGAGGGCGGAGGAGGCGAGAGTGTGTCGAATCTGCGAGTGT
 AAGAGGGGCGAGGAGAAAAGAAACAAAGCCACAGACGCAACTGAGACTCCCGCATCCCAAAGAACGACCCAGAT
 CAGCAAAAAAGAAAGATGGGCCCCCGAGCCTCGTGCTGTGCTTGTCTCCGCAACTGTGTTCTCCCTGCTGGG
 TGGAACTCGGCTTCTCTGTGCGACCCACCGCTGAAAGGCAAGGTTTCAGAGGGACCCGAGGAACATCCGCCCA
 ACATCATCTCGTGTGCTGACGGAGCAGCAGGATGTGGAGCTGGGTTCCATCGAGTGATGAACAAGACCGGCGC
 ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCTTCGTGACCACCCCATGTCTGCCCTCAGCTCTCTC
 CATCCTCACTGGCAAGTACCTCCAAACCAACACCTACACCAACAATGAGAAGTGTCTCCCTCGCCCTCTGGC
 AGGCACAGCAGGAGCGCAGCCTTTGCCGTGTACTTCATAGCACTGGCTACCGGACAGCTTCTTCGGGAAG
 TATCTTAATGANTACAAGGCTCCTACGTGCCACCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCG
 CTTTATACATACACGCTGTGTGGAACGGGTTGAAAGAGAAGCACGGCTCCGACTACCTCAAGGATTACCTCA
 CAGACCTCACTCAACATGACAGCGTGAGCTTCTTCGCGACGTCCAGAAAGATGTACCGCAGCAGGCCAGTCTCT
 ATGGTCATAGCCATGCGAGCCCCACGCGCCTGAGGATTACGCCCCACAATATTACGCGCTTCTCCCAAAGCG
 ATCTCAGCAGATACGCGGAGCTACAACCTACGCGCCCAACCCGAGCAAAACATGGATCATGGCTACAGCGGGC
 CCATGAAGCCCATCCACATGGAATTTACCAACATGCTCCAGCGGAAGCGCTTGAGACCCCTCATGCTGGTGAC
 GACTCCATGGAGACGATTACAAACATGCTGGTTGAGACGGGCGAGCTGGACAACAGCTACATCTGTATACACGCG
 CGACACGGTTACACATCGGCATCTGGCCCTTGCGTTGAAAGGAAATCCATGCAATAGATTGATGATGACGCTG
 TCCGCTTCTACGTGAGGGGCCCCAAGCTGGAAGCCGCGCTGTCTGAATCCCAACATGCTCCTCAACATTGACCTG
 GCCCCACCATCTCTGACATTTGAGGCTGGACATACCTGCGGATATGGACGGAAATGACTCCTCAAGCTGCT
 GGACAGCGAGCGGCGGCTGAATCGGTTTCACTTGAAGAAGAAGATGAGGCTTCTGGCGGACTCCTTCTTGGTGG
 AGAGAGGCAAGCTGCTTCAACAAGAGACAATGACAAGGTTGGACGCCAGGAGGAGAACTTCTGCCCCAAGTAC
 CAGCGTGTGAAGGACCTGTGTGAGCTGCTGAGTACCAGACGCGGTGTGACAGCTGGGACAGAGTGGCAGTGT
 TGTGGAGGACGCGACGGGGAAGCTGAAGCTGCTAAGTGCRAAGGCGCCCATCGCGCTGGGCGGACGACGCCC
 TCTCCAACTCGTGCCCAAGTACTACGGGCGAGGCGAGCGGCTGCACCTGTGACAGCGGGGACTACAAGCTC
 AGCTGGCGGACGCGCGGAAAACCTCTCAAGAAGAAGTACAAAGCCAGCTATGTCCGACTCGCTCCATCCG
 CTCAGTGGCCATCGAGGTGGACGCGAGGTTGACCACTAGGCGTGGTGATGCCGCCAGCAGCCGGAACCTCA
 CCAAGCGGCATCTGCCAGGGGCCCCGAGGACCAAGATGACAAGGATGGTGGGCACTTCAGTGGCACTGGAGCG
 CTCTCCGACTCACTCAGCGCCCAACCCATTAAAGTGAACATCGGTGCTACATCTAGAGAGACGACAGCTCCA
 GTGTGACTGACCTGTACAGTCTCTCGAGGCTCGAAGAGCCCAAGCTGCACTCAGCCAGCATGATGATGAAA
 CCTGCGAGAACAAATTAAGAACTGAGGGAGTCCGAGGTCACTGAAGAAAAGCGGCGCAGAAGAATGTGAC
 TGTCACAAATCAGCTACCAACCGCAGCACAAGCGCGCTCAAGCAGCAGAGGCTCCAGCTGCTGATCTTTGAG
 GAGGCGCTCGAAGAGAGGACAAGGTGTGGCTGTTGCGGGGACGAAAGCGAAGAAACTCCGCAAGAGTGC
 TCAAGCGCCTCGAAGAACGACGATGTCAGCATGCCAGGCTCAAGTGTCTACCCAGCAGCAACGACGATGG
 CAGCGCGCGCTTTCTGGAACCTCGGGGCTTTCTGCTGTCGACCCAGCGCAACAATTAACAGTACTGTGTGAT
 GAGGACCATCAATGAGACTACAATTTCTCTTCTGTGAATTTGCAACTGGCTCTGTAGAGTACTTGTATCTCA
 ACACGAGCCCTCCAGCTGATGAATCGAGTGAACACACTGGACGGGATGTCTCAACAGCTACACGTACAG
 CTCTATGGAGCTGAGGAGTGAAGGTTTACAAGAGTGTAAACCCCGGACTCGAAACATGGAACCTGGATGGAG
 AAGCTATGAGCAATACAGGCACTTCAGCGTGAAGTGGCAAGAAATGAGGACCTCTCTTCCAAATCACTGG
 GACAACCTGGGGAAGGCTGGGAAGGTTAAGAAACACAGAGGTGGAACCTCAAAAACATAGAGGCATCAACCTGA
 CTGCAAGGCAATGAAAAACCATGTGGGTGATTTCAGGACAGCTGTGCTATTGGCCAGGAGGCTCGAGAAGC
 AAGCAGCGCACTCACTCAACATGACAGATCTGGAGGATAACGACGAGGAGCAGAGATAACTCTCAGGAAGTCC
 ATTTTGGCCCTGCTTTTGGCTTTGATTATACCTCACCAGCTGCACAAAATGAGATTTTTCGTATACAAAAGTC
 ACCACTAACCCTCCCCAGAGCTCAAAAAGGAAACGGAGAGAGCGAGGACAGAGATTTCTTGGAAATTTCT
 TCCAGAGGCGAAAGCTCATTTGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCTCTTTATCTT
 TTGGTTTGTCAAAAGGAAGTAAAGAGCAGGACAGGCAACGCTGGAGAGGCTGAAAACAGTGCAGAGACG
 TTTGCAATGAGTCAGTACGACAAAAGATGACATTACCTAGCACTATAAACCTGGTTGCTCTGAAGAAAC
 CTGCTTTCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTAGGGGAACCTAATAGAAT
 CCCAATTTTCAGGAGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNECSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEYFDIRVPFYVRGPNVEAGCLNPHIVLNIIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLQCRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYIENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPCECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMTINETHNFLCFEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCGKYQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGGACTGTCCGGCTCCCAG**ATG**CTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCCTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCACGCCTTGGCCCTTCCGGCGGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGC**TGA**GGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTTCGGGGCTGGACAGCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFRR
RRHGLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

49/330

FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTCACCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCAGAGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGAGCAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGAGCCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCCTCCTTCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGTC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTCACCTGGAAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRsIAVYYDNPHMVPPDKRCrCAVGSILSEGEESpSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRrVHPALDTYIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSpgsRETSAATLSPGAS
SRGWDDGDTRSEHSYSESgASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

0
0
0
0
4
2
4
4
4
0
0
4

FIGURE 52

CCGCGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCT
 GCCCCGCGCCAGTC**ATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCTTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAATTTTAAAAAACTAAAAAAAAAAAAAAAAAAAA

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPECAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYKGRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNRKSKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAAGCTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTTTGTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTGTGTAATACT
 AAAATCACGAGAACCTAAACAACAACCAAAAATCTATGTGGTATGCACCTGATTAACCT
 ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGTCTGAAGATTAAATGTGTTTATTCAAATGTGGT
 CTCCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATTCCTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCGTGAACATGTAAT
 GTAACCTGGCTTTTGGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
22

FIGURE 58

TTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGCGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTG
TTTGGGTCAAACAGGTGNTNGCATTGCGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCGGGAACCATTGACACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACCTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

TGACGCGCGGGTGATGCTGGGCTCCGCTGGTGTGCTGCTCTGGCTGTGCTGCTCTGGCCGTCC
TGTCCAAAGTTTACTTGGGACTTATCTTGGCAGTCTTCCGACAGTCCCCAAGATCTTCTCCGAAGAGTGC
AAAGCGCCCCAGCGCCCTCTGTAATCTGCAAGAGGCGCCAGGAAGGTTCTCTCAAAACAAAGC
TTTTTTCAGCAACCAAGTGCCTGCAAGAGCTGGATGTGGTGTTAATTTGGCAGTGGCTTTTGGGG
CGCTGGCTCGAGCTGCAATTCTTAGCTTAAGCTGCAAGGCAAGTGTGGTGCTGGAACAACATC
ACCAAGGCGAGGGGCTGCTGTACATCTTTGGAAGATCTGCTGGTGTGGAACAACATC
CCATTACATTTGGCGGTATGGAAGAGGCGAGCATTTGGTGTTTTATCTGACAGAGATCACTC
AAGGCGACGTGGACTGGCTGGCTCCCTCTCCTCTCTTTGACATCTGCGTCTGCTGCTGCTG
AATGCGCCAAAGGAATACCCCATGTACAGTGGAGAAAGACCTACATTTAGGCGGCTCAGCGC
GAAGTTTCCACAGGAGGAAGATCATCTATTGACAAGTATATAAAGCTGGTTAAAGTGTGATCC
GTGGAGCCCTCATGCCATCTGTTGAAATTCCTCCCATTTGCCGCTGGTTCACGCTTGTGCGAC
GGGTGTGGGCTCAGTCTCGTTTCTCTCTCATCTTCAACATCCACAGGACGCTGGCTGTA
GGTCTCGACAGCACTGGGGGCTCTCCTTGAGCTCAGGCGACATCTAGCTATCATCTTCCCCA
CTTAGCGTGTACCCCCAAACCAAGTGCCTTTTCCATGACAGCCCTGCTGTACAACCATAC
ATGAAGAGGAGGCTTTTATCCCGAGGGGGTTCCAGTGAATTTGCGCTTCCACACCATCTCCCTGT
GATTACGGGGCTTGGGGGCGCTGTCTCAAAAGGCCACTGTGCAGAGTGTGTTCTGGACT
CAGCTGGGGAAGAGCTGTGGTGTTCAGTGTGAAGAAGGGGCACTGAGCTGTGAACATCTATTTC
CCCATCTGGTCTTCCAAAGCCAGGACTGTTCAACACCTTATGAACACCTTACTGCGGGGAAGCGC
CCGCTGCCCTGCCAGGTGTGAAGACCAACATGGGGAAGGCTGCGCGCCCGGCTTAGGACTGACCT
CTGTTTTTCACTCTGCTCGGAGGCAACAAGGAAGACCTGCATCTGCGCTGCCAACACTACTAT
GTTTACTATGACAGGCAATGACACAGGCGATGAGCGGCTAGGAGCGCTAGCTCTCATCTCCGAGGA
GGCTCGGGAACACATCCCTCTTCTCTTCTGCTTTCCATCAGCCAAAGATCGGACCTGGG
AGAGCCGATTCCAGCGCGGCTCGCCACATGATCATGTCTCATACCCACTGCCCTACGAGTGGTTT
GAGGATGGCAGGCGGAGCTGAAGGGAAGCGGGGCACTGACATGAGACCTCTCAAAGATT
TTTTTGTGAAGCTCTATATGTCAGTGTCTTGAACATGTTCACACAGCTGGAGGGGAAGTGTG
AGAGTGTGATGTCAGGATCCCCACTCAACCAACAGTTTGTACTTGGCTGCTCCCCAGGTTGCC
TGTTCAGGGGCTGACCATGACCTGGGCGGCTGCACCTCTGTGTGATGGCTCTCTTAGGCGC
CCAGAGCCCCATCCCCAACTCTATCTGACAGGCGAGGATATCTCACCTGTGGAATGTGTCG
GGGCGCTGCAAGGTGCCCTGCTGTGCGACAGCGGCATCTGAAGTGAAGTCTGTACTCGACAGC
CTTAAGAATCTTGATTCTAGGATCGGGGCAAGAGAATAAGAGATGAAGTGCATCAGGAGG
AGTCAAGAGGAATTTGCCAATTTGGCTGGGGCACTCTCCCTTGACTTACCATTAATGTCTTTTCTG
CATTTAGTTCCTTGACATGATAAAGCACTTAATTTGGTTGATGCTGAGAGGAGGCGTAG
TTTAAATACAAATTTCCGAATCTGGGGCAATTTGGAATCATGCTTCTCCAGCTGGGGCAGGTGAGA
TCTTTACGCGCTTTATAAGATGCCATCCCTACTAATAGGATATTGACTGATAGTCTGATG
TCTCATGACGAGCGGGCGCTCTGCATCCCTCAGCTCACCATTGCCCTCAACTCAGTGTACAAAGCGA
ATATTCCATCTGTGGATGAAGACCTCTGGCAGTTGTGAGCTCAAGCTGGTGGGTTTCAGTTC
TGTCTGAGGCTTCTGCTCTCATCTATTAGTGCTACGGCTGCACAGTTCTACACTGTGTCAGG
AAAAAGGGGACTTAATGAGGCTTAACCTCAAACCTGGGCGGTGTTTTGGTTGCCATTCATA
GCTGTTGAGACATCTAGATCTCTTTGTGCTGGGTCAGTGGCTCTTCAGGGGACAGGAAT
GCCCTGTCTGGGCTGTGGGTTTGGAGCTTTGGGTAACGACAGGATCATAGTTAGTA
GGGTGCAATCTGATGATGCTGATGCTGATGCTGATGGAATCCCGGCTGTGCTCTCCCTTATCA
TCTGGGCTGCGCAGTGTGTTCTCAATCTGGCCCTCAGGACTCAGTACTGAGCTCTGAGCTCTCATCAGC
CTTATCCACAATAACACAGGGAAGGCTGATGCGAGGAGTGTGACATCAGGAGTCAAGGCA
TGGACTGTGTAAGTGAATCTTTGCTGGCTGAAGCAGTGCAGGCACTACAGGCCAAGG
CACAGCAGGGGACAGTCAGGAGGAGTGTGGGTAAGGAGGAGTGTGAGGAGGAGTGTGAGGCA
AAGCCGCGGAATGTGCTGTAACCCAGAATGGCATTTGCAGCTTAATTAGCACATGTGTTGTTG
TTAGACAGGTAGTGAATGCAGCTCAAGGTTTGGAAAACTCACTTTTCAGTTATGTGTTTGT
GTATCAGACATCAGAAGGCTCTTTTGTAGTTCGTGTTAATGTACATTAAATAAATTTATTG
ATTCCATTGCTTTTAAAAAATAAAAAA

FIGURE 64

MWLPVLVLLAVLLAVLCKVYLGLFSGSSPNPFSEDKRPPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEHLPLSTNYVVYDMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFPRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLSDLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNFENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAKRRQMQAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSR L

66/330
SESELESSIQEEDSLKSQEGESVTEDISFLESPNFENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAKRRQMQAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSR L

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

CGGCGCCGCCCGCCGACACCGCGGCGCGGGGGCGCGGGCGCGCGGATGCGGGCGCGGGGGCGCG
CGATGACCGCGAGCGACGACGCGCGGGCGCGCGCTGACCCGCGCCGCCCGCCGCTGAGCCG
CCCGCCGAGCTCCGGACAGGCGCGACATGACGCGCGAGCGCCCTGTTGCTGCTCCTGCTGCGCG
CGCTGCTCTGCGGGCCTTCCACACCGCGCGCGCGCGCGCGAGGCCCCCAAAGATGGCGAGC
AAGGTGGTCCCAACGGCAGGTGGCGCGCTGGGCGCGCATGTGCGCTGACAGTGGCCAGTGGAG
GGGGGACCGCGCGCGCTGACCATATGTGGACAAAGGATGCCCGACCATTCACAGCGCGCTGGA
GCGGCTTCGCGGTGTGCTGCGCGAGGGGCTGAAAGTGAAGCAGTGGAGCGGGAGAGTGTGCGGG
GTGTACGTGTGTGAAGCGCCACAAAGCCTTCGGCAGCCTTGAGGCTCAACTACACCTCTGCTGT
GCTGGATGACATTGATCCGAGGAGAGAGAGAGCGCTGGGCGCGACAGCTCTCTTGGGGGTCAG
AGGACCCCGCGACGACGATGGGACAGCGCGGCTTCACACAGCCCTCCAAGATGAGGCG
CGGGTGTATCGACGCGCGGTGGGTAGCTCGTTCGGCTCAAGTGTGCTGGCCAGCGGGACCG
CGCGCGCGACATCACCTGGATGAAGGACGACAGCCCTTGACGCGCCGAGGAGCGCGCTGAGC
ACAGGAAGAAGATGGAACCTGAGCTGAGGCTGAAGAACCTGCGCGGGAGACAGCGCAATAAT
ACCTTGGCGCGTGTGCAAAACCGCGCGGCGCGCTCAACCGCACCTACAAGGTGGATGTGATCCAC
CGGACCGGCTTCAAGGCGCGTGCTCACAGGCACGACCCCGTGAAACACAGCGGTGACATTCG
TGAGGACACACGCTCTTCAGTGCAGGTTGCGACAGTGAAGCGGGTGATCCGCTGGTGT
AAGCGCGTGGAGTACGGCGCGGAGGCGCGCCACAACTCACCATCGATGTGGGCGCGAGAA
GTTTGTGGTGTGCTGCCACGGGTGACGTGTGGTGTGCGGCCCGACGGCTCTCTACTCTAATAAG
TGCTCATACCCGTGCGCCGACGAGCATGCGGGCATGTACATCTGCTTGTGGCGCAACAC
ATGGGCTACAGCTTCCGACGCGCCTTCTCTACCGTGTCTGCGAGACGCAAAACCGCGAGGCG
ACCTTGGCGCTCTCTGCTCTCGGCACATAGCTTGGCTGGCCCGTGTGTCATCGGATCCAG
CGCGCGCTCTGCTTCATCTGCGGACCCCTGCTCTGTGGCTTGGCAGGCCAGGAAGAAGCG
TGACCCCGCGCGCTGCCCTCTCCCTGCTGGCAGCGCCCGCGGGAGCGCGCGCACCG
CAGCGGAGACAAAGACCTTCCCTGCTTGGCCGCGCTCAGCGCTGGCCCTGTGTGTGGGGCTGT
GTGAGGAGACATGGGTCTCCGCGAGCCCGACGACTTACTGGCCGAGGCCAGTGTGCTGGC
CTCAAGTTGTACCGAAACTCTACACAGCATTCACACACACACACACACACACTCTCACAC
ACACTCACAGTGGAGGCGAAGTGCACACAGCATTCACATTCAGTGTAGCAGGACCGGT
TGTTCGATGTGGGACCGGGGGGGCGGCCACAGCAGGCAGTGGGAGATGGAGGACGGAGCT
GCAGCAAGGCGAGGGACCATGCGCAGAGGAGTAATGCCACACCCCGACGATCTGTGTGT
TGAGGCATAGCCCTTGACACACACACACAGACACACACACTACCTGGATGCATGTATGCAC
ACATACGCGCGACAGCTGTCTCTGAAGCGACAGTACGCACACGCACATGCACAGATATG
CCGCTGGGACACAGATAAAGTGCCAAATGCACGACACAGCAGACAGAGATATGCCAAGAT
TACAGGACATGCTGCTGCACATACACAGCACACCATGCGCAGATGTGCTGCTGGACAC
CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCGGGACAC
CAGTGTGCACAGATATGCTGCTGGACACACAGATATGCTGCTTGACACACATGCACGG
ATATTGCTGGACACACACACACACACAGCTGCACAGATATGCTGCTGGACAGCAGAC
ACATGCAGATATGCTGCTGGACACACACTTCAGACACACAGTGCACAGGCGAGATATGCT
GCTGGGACACAGCAGATATGCTGTCTATGTCACACACACAGCAGCATGCTGTCCGGACAC
ACACAGCATGCACAGATATGCTGTCCGACACACACACGACGCAGATATGCTGCTGGAC
ACACACAGATATGCTGCTCAACACTCACACAGTGCAGATATGCTGCTGGACACACAC
TGTGCACAGATATGCTGTGACATGTGCACACAGTGCAGATATGCTGTCCGGATACACAG
CAGACACACATGCAGATATGCTGCTGGGACACACATTCGGGACACACATGCACACAGGT
GCAATATGCTGCTGGACACACACACAGATATGCTGCTCAACTCACACAGTGCAGAC
TATTGCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATAT
TGCTGTCCGGATACACAGCAGCAGACATGCAGATATGCTGCTGGGACACACATTCGGGAC
CACACATGCGACACAGGTCAGATATGCTGCTGGACACACGACAGCTGACGTGCTTTGG
GAGGTTGTGCGCTGAAGGCTTCAGTACGTGTGCGCTGAGGCTCATAGTTGATGAGGACTTT
CCCTGCTGCGACCTGACTCCCCAACTCTGCGCGCTCTGTCGCCGCTCAGTCCCGGCTC
CATCCCGCTCTGTCCCTGGCTTGGCGGCTATTTTTGACACTGCTTGGTGGCGCCAGG
AGTCCCTTACTGTGTGGGCTGGGTTGGGGGACAGACGCCCAAGCCTGAGAGGCTGGAG
CCATGCTAGTGGCTCATCCCGAGTGCAATTTCTCCCTTGACACAGAAAGGGGCTTGGTA
TTTTATTTAAGAAATAAAGATAAATATAATATGATGAAGAGAAAGTGGGTTGACAGGAC
TGTGGTCTCTCTGGGGCGGGGACCGCGCTGTCTTTACGAGCTGCTGATGACACACCC
GTACAGGCCAGCACACCCACCCCAACCCCATGTCTGTGTGGCCGACATCTGTGTAATTTTA
TGTAGATTTTGTAGCTGAAGCCCGGTATTAATTAATTAATTTTGTAAACACAAA

MTPSPLLLLLLPLLLGAFPPAAAARGPPKMA DKVVPQVQARLGRTVRLQCPVEGDPPLMT
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLVDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA RVPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKEPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGA EGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWFVVGIPAGAVFILGTL LLWLCAQKQKCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPVGVLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHSHVQC

ACGAGCTGAGGAGGCCCTGCTGAAGACACGGTCACTGGGCTGACGAAACCTCCAGGGGACATATCCAGAGTCA
ATGACTCTCTGGAACACCCACATCTCACTCTTGCCACCTCCACAGGGCTGGGGGAAAGATGCTGGGGAACA
AGGCCCTGGGTGTTCTCTCTCTGGTCTGGAGTGCACATCTGTGTGGGGAGACACAGATCACTCCACCGATCA
CTAAGAGAGATCCAGCTCGGGAAGAGAACCCAGATCTTGTCGAAGACCTGCCGACACCTGGAGAGCCCTGG
TGATGGGACACATGGTTCACAGTCGCACTACCGAGCCGGGAGGGGCACTATGAGCGCTGGAGCCGCAATCGCT
TCTACATGGGGACATGTTATGTCGCCCTCCCTGGGCTGAGGGCTGGACCACTGATGACACATCTGGGGG
GAG
GAACCTCTCAATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GCCCATGGTCTCCCTGAGGAAAGTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
TGGCAGAGATGGTTCGCTGTCAGTGAGGCCAGGACGAGAGGCTGACGATCGATGGGCCAGGACTGTACAGC
CTGTGACCTGACCTGCCCAATGGGCGAGGTGAATGCTGATGTGCTGATGTGCTGCTGCTGCTGCTGCTGCTGCT
ATGGGGCTGTCTCTCTCTCCGAGGTGGCCCGAGCTCAGGGGCTGCTATCTACCTCTGACCAAGAGCGCGGAG
GAG
ATGCAACAAGGCTCAAGTTTCCGCCATTGTACTCAATCTCAACAGAGCTCGAAGCGAGGAGGAGGAGGAGGAG
CAGAGTTTCTGAGGGACGAGCACTCAACATCTGGTGTGAACCTGAGACAAGACGAGGAGACTGGGCAGACG
GTGTTCTGTCTGTGTAAGGCCACAGGAAAGCCAGGCCAGCAAGTAATTTTGGTATCTAATAGCAATATGCT
GGATCTCTCTCTCTCAACAAGATGAGAGCAAGCTGGTGCTGAGGAAACTCGAGCAGACAGAGCTGGGGAGTAC
TCTGTAAGCGCCAGAGGTGTCTGGGGCTGTGAAGTCAAGGTTCCCGCAGATATGTCAACAGATCTGATGAT
ACTCTCAACAGGAG
TCTCTCTACTACTGCTGAGGACGCTGCCCTTTTAAAGCTGTGCAGGGACAGAGGATAATGGGATCAGTGGCTCT
ATCTGTGTCAGAAAGTGTGGGACTTCCAGACAGGAAAGGAGAGTCCAGTCAGTGGCTACAGCTACCC
ACCAAGGTGGCCAGAGGATCGACTCGACGGCGGTGTACGGAACCTGGAGCACTCTGTGGGGGCGCTGTCACTG
TCTGACATGGGGAGCCCATGCGCTTTGGGCATGTGTATCTGGGGAACAGCGCTGTGAAGATGACTGGTCACTA
AGGGGAG
TCTCTCAACAGCCCAAGATGCTGACAGGACATGAGAGGCTGGTGTCTCACTTTGTGGACAGGCTCGAAGAG
TCGGGAAGAGCCCATCAGTTTGAAGACCATGGAGCAACATCTATCCCTCGGGGAGTGGTGGTGTCAAGACC
CGATGGCTCAACCTGGAGATTCATCCGAGATTTCTACAGGCAGAAATGGGGAGCCCTATCAAGTAAAGATGAAG
CCGAGTGTGAACCTCTCGGATCCCGGAATTTTCCAGACAGCAAGCTGCCAGCACTGACCTGAACCTCATCAAT
TGACGAAAGGAGACATCTCCCTCTTCGACAGTATGGCAATGTTCTGTGGGACTTCAGAGATGAGGTCACTCA
CTGCTGAG
TCTGAACCTGTCTCACTCAATCCAGACAGGTTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAGGAACAGGAAGAGACAGCAAACTTCTGGTGGGCAACCTGGAGATCTGTGAGAGGAGGCTTTTAACTCTGG
ATGTTCTTGAAGAGAGCGGCTGCTTTTGAAGTGGAGGCGCTACCGGAGTGAGAGTGTCTGGCTGTGAGAGC
ATCCAGGGGGTGTGTGATCTCCGTGTATTAACCTGAGGCTAGAATCGGCTCTTGTGCCAACCTTAGGCGCTGGGG
CTGCTGAGAGTGTGATCAAGAGGCCACAGGGCGCTGTGTGCTGTGATGAGCAGTCCCTGTATGT
CTGCTGAG
CCAAATGAGATCGGCTCTCCCTCAGGCCATCTCAACAAAGCTCAACTACCTCGGACGACCATGAGATCAAG
GGTTTAAAGAACTGTTTCCAGATTAGATGAGGCAAGCCAAAGCCAGCTCAGCTGAGGAGAGCAATGGGCCCA
TCTATGCTTTTGAAGAACTCCGGGATGTGAAGAGGACCAACCCAGTGCAGCCACTCTCCGCTTCCAGGATTT
GAGGGGAGTGTGATATGACTACACACAGCTGCCCTCAACGAGAGTAGGCCATTAGCTGGAGTGAGAGGAGTATCT
CAAGGAG
ATGAGATGATGAG
AGCACTCGGGACAGGGACCGCAAGTGTCTCAGCTGCTGTCTGAGGATTCAGTGCAGTGGAGTGTCTATGA
TCAGGACGATGTGAGGACCGACCTGTGTGAAGGTCACTCCCGAGGGCAGCTGCCGCTCGAGCGAGTGTGAACCCCA
TGCTGCTGATGAGTCACTGGTCAACCACTGGCACTTGAGTCAACAAAGCAACGAGTAGTACACATGTGGTGGCA
CCCTTGAGCCACTGCTGGCCACCAACTATGGCATCTACACTGTCACCTGACGAGGAGCCCTCGAGCGAGGAGGAG
TCTGAG
TCACCTTCAACTGTCTGAGAGGAGCAAGTAGGCGCCAGAGTGGCTTCCAGTACTCCCAAAACCCCGAGCCAG
TCGCCCTGTCTGAGGCACTGTCCAAGGAGAGTGGCTCGAGGAGGACAGCGAGCAGCAGGAGGAGGAGGAGGAGG
CAGGGTGGAGTGGTGGCTCTCTGAGATTTCTGAGATTGCTCAAGAGCCCTGATCAACCTAAGTTTGTGGT
ACTTCACCCCTCTCTGCCCTCATTTCACTGTGACAGCACTGTGAGACTGATGACCAAACTGTCACTTGTTTAA
TTAAGCACTCTGTTTCTGTGAATTTGTGTTCTCAAGCTCTTACTACTTGTGCTGCTGCTGCTGCTGCTGCTGCT
GAG
GGCCATGGGTAAAACCTCGCACTCAACTGTACTCATTTAAATGCCATTAATGCAAAATATACTCTCTTCTT
TTTGCATGGTTTGGCCACTCTGCAATATGATGATAATCTGATGTGAGATCAAAATAACCAATATAAGATATA
TCTTGGCCTGTGCTCCACAGGCATAGGCAAGCTTGATCATATTTATCATATATAAATGGTGTGAATAAAG
AATAATAACAATAATTTTACTTGAATGTAAATATATTTATTTTCTGCTAATTTTGGAAATCTGTAGTG
ATCATCAATTAATCAAGCTGTGATATTTTCTTACTCTTCTTCCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCT
CCAGTGTGCTCCAGGCGAGATGCTAATAAATGTCATATCTTATTTTCAAATAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPEGFWCLNREQ
 RPGQNCSNYTVRFLCPPGSLRRDTERIWSFWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCMPGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
 TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPESYLIRLPHDCFQ NATNSFY YDVGRCPV
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRC TETR SIVRGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGS AVFHEIKMLRRKEPIT LEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV
 KASVTFLDP RNISTATAAQ TDLNF INDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKV RAYRSE RFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVP AFCDQSPDAYSAYVLAS LAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
 VKKTA FQISMAKPRPNSA EESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
 EDDPMSWTE DYLA WWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKV I PQGSCRRASVNPMLHEYL NVNHLPLAV
 NNDTSEY TMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVP SRRQQRASRGGRQGGVVASLRFRPRA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCCTAAACACACAAGTATGTTAGGCTTCCACCAAAGTCTTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTTCATATTTGGTCTTGGGATCTGCTTTGAGGTCCCATCTTCATTATAAAAAAAATACAGAG
 ACCTACCTACCCTACGCATACATACATATGTTGTATATATGTAACCTAGACAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGATGATTACAAAGAATTTAGACATGTTATTGTCAGAGTCCCTCTCGATTTCATG
 CCTTTGGTTCACGGTCTCCTTCAGTGTATGCAGCCCTACCCCTTTGGTTGGGGACATATGATTTGTGTAAAGCT
 CAGATTTACACGGAAGAAGGGAAGTGGGATTACATGGCCTGCCAGCGGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTCATGTGCAATATGAGTGTGATGCGAGTACCCCTGAGCTGGCAGACCCCTGAGCTGATGTTTGGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGAGCAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTTCACACAGA
 AGAGTACTCAACAGGGTATACAAACAATAGCAAAATAATCCACTTTGAAATCAAAACAGGTTCCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTT
 ACAGTCAAGACCTGAGGATAAGGCTGTTAAGACACGCCGTTGGGGAAATATTTGTAGATGAGTACACTTGGC
 ACGCTACTTTTACGGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGACGTGCCACA
 ACAAGCTGCGCTGCTGTGCCCCGGCCGATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGGCGCCCGCCGACGGCACCCAGCGCTGCTGCTGCTGACCAAGCTGCT
 GGGAAACCGCCAGCCCCCTGGTGTCTAGGTGTCACCTCCAGCCACACCGGACGGGCTGTGCGCTGGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAACTAAGCCATATTTATCACCGTGGGACAGACATCCGAGTCAAGACTGTAAATTC
 TGACTCCAGGAGTGTGGCAGCTGTTGATATTATCACTGCAAAATCACATTGGCAGCTGACAGACATATTGTTGA
 TTGAAAGGCTGCGACAGCCCCCAACAGGAAAGCAAAAAACAACAAATCAACCGACTAAAAACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACAAACAAATAGCATTTCTTTCGTGTGAG
 GTGCTTTGTGGGATAAGGAAATCTGTTACAAGCTGCCATATTGGCTGCTTCCGTCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAGATTTCTTTGCTGATGTAGTGTGCAAC
 TGTGTAAACAGCCCCCTCTAAAGGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACCCCACTATCAAGAGTGGCTATAGGAAAAAAGAAAGTGTATCTATCCCTTTGTATTCAATGAAGTT
 ATTTTCTTGAACCTACTGTAATATGCTAGATTTTGTATATTGCCAATTTGGTTTACACAGCAATCTGTAAAT
 GTATCTAATTGAAATCAGCAAGACTGACATTTTATTTTGTCTCTTTCTGCTTCTGTTTGTTCCTGCTGACAG
 GATTTCTCTTAAGGGCAACAGCTGCTGGCATCAAGAATATCAGTTTACATATATAACAGTGTAAATGAA
 TTCCACCAAGGACATTTCAATGTTTCTTCTGCTTTAACTCTGGAAGATTTAAAGAAATAAAACCTCTGCA
 TAAACGATTTCCAGATTTGTATTGCAATTTCTTAAGATGAAAGGAACGCCCAAGCAGTTTCCACACTCACT
 TTAAGTATTTCTGTGGAGTGTGATCATTGAGTGTGAGCAATTTAGTTCACGGAAGATGGATTGATGTTCACT
 AGCTTGGCAACTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACACAGCAAAAAA
 AAAAAA

MYLSRSLSIHALWVTSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNIITLSWSKTIETLTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYATDCLDAF
HMDPKSVKDL SQHTVLEI ICTEEYSTGYTNSKIIHFEIKDRFALFAGPRLRNMA SLYGQLD
TTKKLRDFFT VTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKN LHATVCVYDN
SKLTCECEHNTTGPDCGCKKNYQGRPWSPGSYLP I PKGTANTC IPSISSIGTNVCDNELLH
CNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGGAPPHGT PALLLLTTLTGTA S
PLNG

CCACGCGCTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGCGCG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGCGCGCCGTCCGGGCGAGGTGTCTCTCATGACTT
CTCTTGTTGACCATGTCCGTGATCTTTTTTGCTTCGCTGGTACGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTTCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTTGAGACCCCTGTGGTGGGAATTACAGCTTCCATGACA
CTACTGCAATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGTCACACACCGATGCACTTGGAGCCTGCTCTCAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCTCTCCTCATTTCTCAACATCATGTGTGCTGCCCTGAATGTA
CATTCGAGGAGTTTACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACTCGTGAAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT
TCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTGTATCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAGCATAAATACGTAGGCTGATTTAGTCAGGGGCAAAACCAT
TTACTTTACATATTCTGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
TTGTAACAATAAATATTTTGAGTAAATATGGGTACATTTTAAACAACTCAGTAGTACAACC
TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AAGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAA
AAAA

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAAGGGAGGACAGAGCCCTTAAACAGAGGCGGGTGGTG
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGAGGCTGCCAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGCCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCT
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCGGAACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCCTCATGCCCTTTGCATATTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCCGATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGGTGGTGCTGACCG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGTCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCGGTCACTTACGGTTGTACTCATCTTTACCTAATGGGTGCTCAGTGTGGGGTTCTATA
 GCTCTCACTCTTCCGGAGCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCTGGTCTAAGCTCAGCACTTCTGTCTCTCTCGAACCCTGGG
 GCTCACTCGCTTTGACCTGTCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCGAGCCTTTGCAAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCCGT
 CTCGGTTTCCCCAGGCATCTAGGAAGACCAGCACCAGTGACACTCCAGCTGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCGCTGGAGGGAAGCCCCAAGGCTACTTGG
 ACCTCAGGACCTTGGAAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATTT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACGTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGTGATGTGCAAT
 AGGGTGGGTAGGGGAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCTC
 CTTGCTCTGGGCCAGCAGGCCCTAAGCACTGTGCTATCCTGGAGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK
IALELCFTFLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPQGTSLGQVSFSLGSGFAGVIVVLIFYLMVSSVVGIFY
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY
IVFLYNAAFAGLTTLCVKTFTAAVRAELIRAFGLDRPLPVS GFPAQSRKTQHQ

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCTCTCCCGGGCCACAGAGCACTCGGCTTACGTATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCACGAGAGGATCCGCGAGTGTA
TTATATCAACATCTGTTTGCAACACTGTACATCTCTGCCACATCTTCTGACCCGCTTC
AAGAAGCCTGCTGAGTTACCAACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNCCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTGGTGGTCCAGGTCTT**CATGCT**GTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCA GTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCAC TTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAGG**CCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGFPHAAQANVELLGSSDLLT

☐ 1. ☐ 2. ☐ 3. ☐ 4. ☐ 5. ☐ 6. ☐ 7. ☐ 8. ☐ 9. ☐ 10. ☐ 11. ☐ 12. ☐ 13. ☐ 14. ☐ 15. ☐ 16. ☐ 17. ☐ 18. ☐ 19. ☐ 20. ☐ 21. ☐ 22. ☐ 23. ☐ 24. ☐ 25. ☐ 26. ☐ 27. ☐ 28. ☐ 29. ☐ 30. ☐ 31. ☐ 32. ☐ 33. ☐ 34. ☐ 35. ☐ 36. ☐ 37. ☐ 38. ☐ 39. ☐ 40. ☐ 41. ☐ 42. ☐ 43. ☐ 44. ☐ 45. ☐ 46. ☐ 47. ☐ 48. ☐ 49. ☐ 50. ☐ 51. ☐ 52. ☐ 53. ☐ 54. ☐ 55. ☐ 56. ☐ 57. ☐ 58. ☐ 59. ☐ 60. ☐ 61. ☐ 62. ☐ 63. ☐ 64. ☐ 65. ☐ 66. ☐ 67. ☐ 68. ☐ 69. ☐ 70. ☐ 71. ☐ 72. ☐ 73. ☐ 74. ☐ 75. ☐ 76. ☐ 77. ☐ 78. ☐ 79. ☐ 80. ☐ 81. ☐ 82. ☐ 83. ☐ 84. ☐ 85. ☐ 86. ☐ 87. ☐ 88. ☐ 89. ☐ 90. ☐ 91. ☐ 92. ☐ 93. ☐ 94. ☐ 95. ☐ 96. ☐ 97. ☐ 98. ☐ 99. ☐ 100. ☐ 101. ☐ 102. ☐ 103. ☐ 104. ☐ 105. ☐ 106. ☐ 107. ☐ 108. ☐ 109. ☐ 110. ☐ 111. ☐ 112. ☐ 113. ☐ 114. ☐ 115. ☐ 116. ☐ 117. ☐ 118. ☐ 119. ☐ 120. ☐ 121. ☐ 122. ☐ 123. ☐ 124. ☐ 125. ☐ 126. ☐ 127. ☐ 128. ☐ 129. ☐ 130. ☐ 131. ☐ 132. ☐ 133. ☐ 134. ☐ 135. ☐ 136. ☐ 137. ☐ 138. ☐ 139. ☐ 140. ☐ 141. ☐ 142. ☐ 143. ☐ 144. ☐ 145. ☐ 146. ☐ 147. ☐ 148. ☐ 149. ☐ 150. ☐ 151. ☐ 152. ☐ 153. ☐ 154. ☐ 155. ☐ 156. ☐ 157. ☐ 158. ☐ 159. ☐ 160. ☐ 161. ☐ 162. ☐ 163. ☐ 164. ☐ 165. ☐ 166. ☐ 167. ☐ 168. ☐ 169. ☐ 170. ☐ 171. ☐ 172. ☐ 173. ☐ 174. ☐ 175. ☐ 176. ☐ 177. ☐ 178. ☐ 179. ☐ 180. ☐ 181. ☐ 182. ☐ 183. ☐ 184. ☐ 185. ☐ 186. ☐ 187. ☐ 188. ☐ 189. ☐ 190. ☐ 191. ☐ 192. ☐ 193. ☐ 194. ☐ 195. ☐ 196. ☐ 197. ☐ 198. ☐ 199. ☐ 200. ☐ 201. ☐ 202. ☐ 203. ☐ 204. ☐ 205. ☐ 206. ☐ 207. ☐ 208. ☐ 209. ☐ 210. ☐ 211. ☐ 212. ☐ 213. ☐ 214. ☐ 215. ☐ 216. ☐ 217. ☐ 218. ☐ 219. ☐ 220. ☐ 221. ☐ 222. ☐ 223. ☐ 224. ☐ 225. ☐ 226. ☐ 227. ☐ 228. ☐ 229. ☐ 230. ☐ 231. ☐ 232. ☐ 233. ☐ 234. ☐ 235. ☐ 236. ☐ 237. ☐ 238. ☐ 239. ☐ 240. ☐ 241. ☐ 242. ☐ 243. ☐ 244. ☐ 245. ☐ 246. ☐ 247. ☐ 248. ☐ 249. ☐ 250. ☐ 251. ☐ 252. ☐ 253. ☐ 254. ☐ 255. ☐ 256. ☐ 257. ☐ 258. ☐ 259. ☐ 260. ☐ 261. ☐ 262. ☐ 263. ☐ 264. ☐ 265. ☐ 266. ☐ 267. ☐ 268. ☐ 269. ☐ 270. ☐ 271. ☐ 272. ☐ 273. ☐ 274. ☐ 275. ☐ 276. ☐ 277. ☐ 278. ☐ 279. ☐ 280. ☐ 281. ☐ 282. ☐ 283. ☐ 284. ☐ 285. ☐ 286. ☐ 287. ☐ 288. ☐ 289. ☐ 290. ☐ 291. ☐ 292. ☐ 293. ☐ 294. ☐ 295. ☐ 296. ☐ 297. ☐ 298. ☐ 299. ☐ 300. ☐ 301. ☐ 302. ☐ 303. ☐ 304. ☐ 305. ☐ 306. ☐ 307. ☐ 308. ☐ 309. ☐ 310. ☐ 311. ☐ 312. ☐ 313. ☐ 314. ☐ 315. ☐ 316. ☐ 317. ☐ 318. ☐ 319. ☐ 320. ☐ 321. ☐ 322. ☐ 323. ☐ 324. ☐ 325. ☐ 326. ☐ 327. ☐ 328. ☐ 329. ☐ 330. ☐ 331. ☐ 332. ☐ 333. ☐ 334. ☐ 335. ☐ 336. ☐ 337. ☐ 338. ☐ 339. ☐ 340. ☐ 341. ☐ 342. ☐ 343. ☐ 344. ☐ 345. ☐ 346. ☐ 347. ☐ 348. ☐ 349. ☐ 350. ☐ 351. ☐ 352. ☐ 353. ☐ 354. ☐ 355. ☐ 356. ☐ 357. ☐ 358. ☐ 359. ☐ 360. ☐ 361. ☐ 362. ☐ 363. ☐ 364. ☐ 365. ☐ 366. ☐ 367. ☐ 368. ☐ 369. ☐ 370. ☐ 371. ☐ 372. ☐ 373. ☐ 374. ☐ 375. ☐ 376. ☐ 377. ☐ 378. ☐ 379. ☐ 380. ☐ 381. ☐ 382.

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGGCGGAGGAGGTGTGAG
 GAGTGTGTGGAAACAGGACCCGGGACAGAGGAACCAATGGGCTCCGCAGAACCTGAGCACCTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCCCTCGAAGTGCTCTATAAAGGATATTAAAAAGGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACCTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAACTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTCGAGAGTG
 AATAAAATTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGATGACC
 AGCAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAATACATTTTGTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
 DRNIPRGSDIIVDLEVITLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGMETPFIFGEGEPHV DGE PGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGAAACA
GTACGATAATTATGGTGAAGAAGGATTTAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGACAGAGGCGGCGGGGAGTGC CGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAAGTGTGCTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTTGGTGCCATGGAGACCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTGAAGATTGTGCACACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGTCAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTGCGGTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTGTCAGGAGCAGTCTGCAATTT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCGTCAGTTTATGCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTCAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTTAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAAGAAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAAC
 ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTTACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 89

GCTTCATTTCTCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTGTTCTTTGGAAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGATTTGTAGTC
 CTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTTGTTCAG
 GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAAGTTGGAGAAAGCAACAATATGGTA**TAA**CAACA
 AGTGAATTTGAAGACTCATTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCGTCTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTGAAGTGTCACATGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCAATTTAAAGTATTAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTNGNCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFPPVVVGFIIRRVVVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

90/330

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCGAGGTGCTTTCGCCGTGTCCCCACCACTGCAGCCATGATCTCCTTA
CGGACACGCAGAAATTTGGAATGGGATTAACCGGATTGGAGTGTTTTCTCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAAGACATTAGATTTCTTCTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTTCTGGGTGGTGATTGTAGTCCCTATTGGTGGCCTTTGATAGGCATG
ATCTCGAAATTTAATGAGATTTTCTTCTCTGTTTC

FIGURE 92

GGCAGGAGGCTGAACCCAGCGGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCTTCTGAGTCCTGGATCTTTCTTCTCTTGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
 TGAAGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
 ATCAACACCATTAGCTCTTCACTCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCAGGAATGCACCATCTTACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGACGACCTCCGGGACTACCCGAGAAGTATTTTTTCTCT
 GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTAGAAA
 TAATGAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
 GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCTTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCTATGTCTTTAGTGGGCTTTGGTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAAGTTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCTTTCATCTTTGTGTGCTGAGTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAGTGTCTTAGTGAGATGACTAAATATGCCTC
 CAAGAAAAAAATTAAGATGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFATVRSRLRVVSAVYDCTLNFRNNENPTLLGVINGKK
YHADLYVRRIPLEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRREWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCCGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAACACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCTCTTTAAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCGAGCACTTAGGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAATAAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAAAAATTCCTTAAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTDSDTGEGFLLGEVKGAEAKNSITDSQMDDEVVYITIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVAVNLGMSQELGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIKQDPQENIFLCQALRITFFPNSEFLHSCVMSLKNRHVSKSS
CNRNHHLDVVDNLTLMVEHTDIPEASPAFTQCIHKKALDLDWRWQFKSRLLDTQDKRKA
NTGSSNQDKASKMSSPTDEIEKMKGFGEYSRIPTF

FIGURE 96

GGCCACAGCCGCGCGGCGGAGGGGCGAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCGAGGCGCAGC
 CCAAGCAGCGCGCAGCGAAGCCCGCGCCGCCACACCCCTCTCGGGTCCCCGCGGGCGCTGCCACCCCTCCCT
 CCTTCCCCGGCTCCCCGCTCGCCGCGCAGTCAGCTTGGCGGGTTCGCTCGCCCGGAAACCCCGAGGTCCACA
 GCGCGCGCTCTGCTTCCCTGGGCGCGCGCCGCTCCAGCGCTCTCTTCCCTCGCCCGCGCGCTGGCACC
 GGGGACCGTGGCTGAGCGGAGGCCACAGTCTACTTTTCGCCCGCGCTCTCTCGCGCTGCTCGCTCTTCCAC
 CAACTCCAACCTCTTCTCCCTCCAGCTCCACTCGCTAGTCCCGGACTCCGCGCAGCCCTCGGCCGCTCCGCTAG
 CGCGCTTCCGCTCCGCTCCAAAGGTGGGAACGCTCCGCCCGCGCGCACCAAGGCGGTTCGGCTTGGC
 CGCGCTTCTCGCACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGGCAGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAAGCAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTCAAGTACAAAGATTG
 ATGAATTTCTCAAAGAACTACTTGAAGATGCAGAGAATCCCTGAATGATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAACGTTACTACGTGGTGGGAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTACAGATGAGTATCTGGAATGTGTAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCTT
 CGCAAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGGCTCTCGTGCTGAAGCCATGTTACAACACTACTGCTCAAAACATCATGAGAGGCTGTTG
 GCTCCCACTGCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAAACATCATGAGAGGCTGTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTTCAACATGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCACAGCTGGACGAAT
 TCTCGTTCATCTCTGAAAGTGCTTCAAGTGTCTGCTTCAAGCAACATCAACCCGAGGAACGCCAACCCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGGCAGAAATTTCTGGTCTC
 CCCTTCCGAGCAAGCTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGG
 AAAGGCAAAAGCAGGTACCTGTTTTCAGTGACAGGAATGGATTAGCCAAACAGGGGCAACCAACAGAGGTCCA
 GGTTGACACCAGCAAAACAGACATACATGCTCTGTCAAATCATGGCTCTTCAGTGATGACCCAGCAAGATGA
 AGAATGCATACAAATGGGACGACGTGGACTTCTTGATATCAGTGATGAAGTAGTGGAGAGGAGTGAAGTGA
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGAATGACATGCAATGCCACTGACCATGCTGGGAGAGTGAAGTGA
 GAAAGCCGACAGTGCTGGTTCGCTCCTGGGGCACAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTCTCTGG
 TTATGTCAGAGAGTGGAGTAATTTCTCAACCTCTGAGAAAAGTGTTCATCAAAAAGTTAAAAGGCACCAAGT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAAACATGTACAGTTTTTACTATGTGCGC
 CACTGGTTTAAAGATGCTGACTTTGCTTTTCTCATTCAGTTTGGAGGAAAGGGACTGTGATCTGAGTTGTTGA
 TCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACGAACTAGGTAGTTGTGCTATTTGTGA
 TTTTATCACTCTATTATTTTGTATGTTTCTCATTTGCTTTGTGGGTTTTTTTCCAACTGTGATCT
 CGCTTGTGTTCTTACAGCAAAACAGGGTCCCTCTTGGCAGCTAACATGATTTTCTGAAATATTAAATA
 GCTGTACAGAGCAGGTTTTATTATCATGTTATCTTATTAAAAGAAAAGGCCAAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
 GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMF
 VKTYGHLYMQNSSELFKDLFVELKRYVVG NVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
 LECVSKYTEQLKPFQDVPRKLKLVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
 LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWN NFIDAMLMVAERLEGPFNIES
 VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGGPPKPLPAGRISR SISESAFSARFRPHHPEE
 RPTTAAGTSLDRLVTDVKEK LQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSR YLF
 AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMK NAYNGNDVDFDISDESSGE
 GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC
TCTAGTGTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRRLTVVLGLLVLF LTCYADDKPKDPDDKPDGSGKDFKPDFPKFLSLLGTEIENAVE
FILRSMRSRSTGFMEFDDNEGHSSK

101/330

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCACTCCTGCAGCTGCTGGTGTCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGTCTGGGCTGTCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTACGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT**TAG**CAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT
 CTCTAGGAAGTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCCAGGAGAAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLQLLVLLLTPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLT KSMAENRHLQYERFVV
APGEDMRQLADGSM DVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVFEP TWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIY LPLRGT

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAA
 AAGTAAAGGAGGATCTTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGAATTTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAAATGGAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCAGTGCTGGAACGATATTACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAAACAGGCAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAGAATTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAGAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALLFLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVVIAASEDRLGGAIAAINSIOHNTRSNVIFYIVTLNNTADHLRSWLSNDSLKSIRYK
IVNFDPKLLEGKVKEDEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRVAGNYSYIGLYDQKKERIRKLSMKASTCSFNPQFVFA
NLTEWKRONITNQDLKWMKLNVEEGLQNTLAGSITTPYLLFVIFYQKSHSTIDPMNVNRLHS
SAGKRYSPQFVKAALKLHWNHGLKPWGRFASYPDVEWKYIIPDPTGKFNLLRYFTEISN1K

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTGAGCACAACACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGCTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCATTGCAGCTATAA
 ACAGCATTCAGCACAAACATCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGAAACGCAGAAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACGATATTCACCTCAGTTTGTAAAGGTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCCAAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAAATTTGAAGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAATTCAAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTTCATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTTGCCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCTATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAAAGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCTGCTCCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAA

09071-1101

09071-1101

09071-1101

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCCTAAGTGGAA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCACTACCCACCTTCTGGTTCACATTTTCATTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGTTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTGCTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCAGGTTATGGAAGGCGGCAAGTGGAAATAAGCCCT
 TTCGGGCATTCCGTTACATGTGGTCTGTAACATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGTCATTTTTAATCTCTGTGGTGAGGATTCGGAGAATCATGTGCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGACTCATGGCTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCC
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCATTTTCTGTGTTTGGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTATCTTCTCCTCAAAA

MSGRDTILGLCILALALSMMAMFTFRFITLLVHIFISLVILGLLFCVGLVWVLYDYDTNDL
SIELDTERENMKCVLGFIAIVSTGITAVLLVLI FVLRKRRIKLTVELFQITNKAISSAPFLFLQ
PLWTFAILIFFWVLVWVALLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFTCSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGLETVALDR

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSQNRPRADPGIQ
RQDPGGAAFQKPVGADVSLGLVPKEELSTQSLPVS LGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVVRVCDTDLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
AGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAACTCC
 TCCCAGCCTTTTCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCGGTGTTGGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAGGGGACT
 GTGTCCATGCCAGTCTTCAGTCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAAGCGAGAGGGCTACCCA
 CTTGCGCCAGAAGTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATACCCCTATGGGGAGTGCATCCTGGGGCTGGGGGTACAA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTGCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATAAACCACTGGATAATTTTTTATTTTATTTTATTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVVQMYKGTVSMPVFQSLEAYWPLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTGGAAGAAACAATGTTCTAGGTTCAAACCTGAGTCTACCA
AATGCCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTGCCACTGTTCTGTGGAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCCTCCAGACACCTTGAAATAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGTGGATGCCTGTGCCACGGCTGTGATGTCTCTGAGGAACCTCCTCAGGECCTGGAT
 CTCA**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGTCTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQFTFMVLEEIIWTSLFMFWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSFVIAPGE
TVVYYSVEYQGEYESLYTSHIWIIPSSWCSLTEGPECVDVDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALFAFVGFMLILV
VVPFLVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACAGAGTCTACCAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTTCGCGCGCAAGGG
GTTNGCGAACCCTTTCGGCGCCTGGGGTATCTCTCGAGAAAAGAGAGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGGTGGCGGCACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCTTGCAACCAGTTTGGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
 AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAACTTGTCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRD LGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQTALVRKLILLKREDL

120/330

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATGG**CTGTCTACGTCGGGATGC
 TGCGCCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCTAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTACGGGGTGACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCCTCCTGAGCATTTGGCCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTTGAAGCAGATCT
 GTCCAGAAGTGGAGAAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTCTGTCTGCCATG
 ACCCCATCAACATCCAGTTACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTAGGAGAGCGCCTGAAACTCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCAACCCTGTACCATTGCTTGGGTTCGTTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCCTCATCTCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCAGCAT
 GTTCGTGGACATTTGAACACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCCTGACATTCGCGCACTT
 CCTTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCTTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAGGCTGAACACGCCCCGGGAGCTGTGC
 ATCCGAGGGTACTCGCTCATGCTGGGCTACTGGGCTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCGAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTCCGCTGAAGGACGGGGAGGAGACCCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAAGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAACAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCCCTGCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGACCCAGTTTC
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAACATAAGAGCTCCTGGATGGGTC
 CGGGAAGTCTGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCACGGCCCTCCCTCTG
 TCCATCCCCACATTTCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTCTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEV DKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLV VAYGTTENSPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGCFCKIVGRSKDMIIRGGENIYPAELEDFHHPKVQEVQVVG VKDDRMGEEICACIRL
 KDGEETTVVEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCTCTGCCTCTCCCATTCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGGCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCCTGACATTTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGCAGGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGACATGTGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGGCGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCGGTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCACCCCTTGTCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACCTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCCATGCCAGCGCCAACAGTCAAGTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTACAGGCAGTATCCTGCAAAAGGGGGGCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTT
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCCGTTTTTCCAACATTCCC
 CAGTATCCCAGCTTCTGCTGCGCTGGTTTGGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAAGTGTACGCGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCCTACTCACTTCTCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGTGGGACAAATGGCTCCCCACTCTAAGCACTGCCTCCCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

MDPARKAGAQAMIWTAGWLLLLLLRGGGAQALECYSCVQKADDGCSPNKMKIVKCAPGV DVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASHVYKGCDFGNVTITAA NVTV
SLPVRCGVQDEFCTRDVGTGPGFTLSSGSCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTISTTSTASFPVRTSTTKMPAFTSQTPROGVEHASDEEPRLTGGAAGHQDRNSNG
QYPAGKGGQPPHNKGCVAPTGLAALLLVAAGVLL

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTQVQPSGGSLWNLRRLLLEPLDANVDA

FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTTCCATCCAAA

FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPKLGKLSATPDAQ



FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTT
TTCTCCAGCCAGTTCCAATCAGGAGACAGGTCCCAAGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAGTATTTTTAGAACTACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACATATTAATTGTAACGATTAATAAAGAATAAGAGCAGCGAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGGAGTATATTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPVTQETGPKAMGDLSCGFAGHS



FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCGCATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTTCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAATAAGTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGGCTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAACTTGTTGATGCAGAATACACAAAAAC
 CAGGCTCGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCCGTGTGGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAAGTGAAGTATAGTATGATCATAGGACCATAGTCCCTCTTTGTGGCA
 ACAGATCTCAGATATCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGTGACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCACTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTTGGAGCAGAAAATTCGTCACTTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAATTTATCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYREND CMFPSCRSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYL FNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKFPVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**GGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCAGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGTACTTTGGGGTCCTCAG
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACAGTGGTGTATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCTCTACCTGGGCCTGGCTCAGGGCTTGATCAGCAAGACCTCCGTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGAGGCAGAG**T**
GAGGAGACTCACTCTGGTTACAAGCCCTGTCTTCTCTCTCCACTGAATCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATTCAGTTTCAGCCA
 CTGAATCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTACTTGCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGTTCCTACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGATTCTCCTGCTCTTAAGTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAASFILAFGTGVEFVRFTSLRPLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLLVFGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLVVVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGACTCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAAACAACAAAACCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTACCCCGAGTGTAAGAACCCTTCGGCTCGCGTGCCTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACCTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGCTACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAACGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGATATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAACCAATCATATTCAGAAGA
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCAGAAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGTACTGTGGAAAATTCATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 GTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTATTATG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATCTTTTACATGCAACATTTTCCAGTTACTTAAGTATGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAGA

MASALWTVLPSRMSLRSLKWSLLLLLSLFFVMWYLSLPHYNVIERVNWMMFYEYEPYIRQD
FHFTRLREHNSCNSHQNPFLVLIVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGD IIRQDFLDTYNNLT LTKIMAFRWVTEFCNPAKVVMKTDTDVFIN
TGNLVKYLNLNLNHS EKFFTGYPLIDNYSYRGFYQKTHISYQEYFPKVFPPYCSGLGYIMSRD
LVPRIYEMGMHVQKPIFEDVYVIGICLNLLKVN IHI PEDTNLFFLYRIHLDVQCQLRRVIAAHG
FSKEIITFWQVQMLRNTCHY

FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGACTATGGATTGTGGACATTT
CCTTCTGTGGAGACCGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNAGSQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTIVHKMNKEVMPSTIQSLDALVKEKKLQGGPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAACTAATCGTGTGAGAAATGACTTTGAAAAGCATTGCTTTTTTACAGAAGTATA
 TTAACTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAAGCTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAGAGTAGAAAAAGAAAAGTAGCCTTACAAGAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCAAAAGCCCTTACAATGGTGTAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCCTCTA
 GGTCTCTAGAACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAGGAAATAAAATACAAAT
 CTTGTTTTTCTAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIEITRLRY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

141/330

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTATAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNNTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATAAAAGCAAAGGGATT
GAATCCGGATGGAACCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGACCGCGTTCTCGCACGCGTCATGGCG
GGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGCAAGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGCTTCTTCTGGAGTACCAGTGG
TTTGTGGACTTTGTGTGTACTCGGGCGCGGTGTACCTCTTACAGAGGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTGTACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCCTTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGCCCCAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCTCACCTTCCAGGCCTGCGGCTGGC
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACAGCTTCTGTCTCCCCGTGTTATCCTGTGGCTCTGGACAAGGCCATTGCACGGGAC
TTCTTGACACGCGCGGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGTTGCTGCTGGTGGTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCTACCTGTGCTGGCCAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCGGG
GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
GGACGGCTGCTGCCAGCTGCTCGCCAGCCTTTTGGCCCTTACTTCCACCAGCACTTGGA
GGCTCCTAGCTGCTGCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGACA
CTAGCCTGCCCCCTCTGTTTGGCCCCCGTGTCCCCAGCTGCAAGTGGGGCCGGACTCCCC
GGCGTTCCTTACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAAGTGTCTCTCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGTGCTGGCTGCTTCTTGAACAAATAAAGGAGCATGCC
GATTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFTSIKMELTVTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIKRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVOQQTARI
AGALGGLTPLFLRGVLAYLIWWTAAQQLLASLFGLYFHQHLA

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTACGACCGTGGATGCCCTGGTCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTCCTTCTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGGCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGCGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCCTGGCTCAGTCTCTGCTAACTACATTGACAATGTGGGCAACCTGCATCTCCTG
 TATTGAGAATCTGTAAAGGTGCTCCCACTACGGGCTGACCAAGATAGGAAGAGGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCAGAGCCACGGCTCCCTCCCAAGAGTTCTTGCAGCTGCGCCACTCTCCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTTGCTACGTGTCTCGGAGAGGACGGGCGAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCCAGGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTCCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAAACATGCCAGCAGG
 CGAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAGGTTGTACCACCTGATCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGCCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGCATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGCGTCTCTCGCG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACGAAGTCCCGCAGCAGGAACAATGGACAGGGCCC
 GGATGCCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGGTGTGTAGCCATCAATGGACATGATCTTGCATATGGCAGCCAGAAAG
 TCGCGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCGCGAGGTTCGGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCATCTCAATAATTACTTGTCTGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTGCAGGGGGAGCATCAGTAGAGAATGGGATTGCTCATCTATGTGCATCAGTGTGTAGCCCG
 GAGGATCATAAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTTGAATGGATGGGTGCAATGATGACA
 GAGTGCAGCCGAGTGAGGCAGTGGCATTATTGAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGATGATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGTGGAAATTACACGGTGTGTATACTGTAAGATATTGTATTAT
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACCCAGCATACAATGATGGAAGAAATAGTGTGGTGATATTTCTCTTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAATATTGTTTCTGGGCTGGCCTTTTTCATGAATCAATGATGGTCAAGGAAAAACAGAAAA
 TCACAAATAGGCTAAGAAGTTGAACACTATATTTATCTTGTGAGTTTATATATTTAAAGAAAGATCAATGT
 AAAAATCTGAGGAAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAAAATATGATCCAAAAAATTA
 AAACACTAGTTTTTTTTTCAGTGTGGAGGATTCTCATCTACACATGTTTATATTTTTCTATTCAAT
 AAAAAGCCCTAAACAACATAAATGATTGATTGTATATCCCACTGAATCAAGCTGATTAAATTTAAATTT
 GGTATCTGTGAAGTCTGCCAAGGTCATTAATGGCCATTTTAAATTTACAGCTCAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACCAAGATAAATATTTTTCAGAAGTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSP EVSAAA TISLMTDEPGLDNPAYVSSAEDGGQPAISPVD SGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVSQRQR
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATCTTTTCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATATA

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

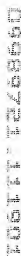


FIGURE 150

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGGAAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGAGGCCCCAGGTGGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCACCTATCACCACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTTCAGGATAGGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESFILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
 CTAATGTCAACGGCCTGGAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAAGATGAAAGAAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
 AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGTACCAAAGGCTCCTGTGAGCAGC
 GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTCTTCTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAAATTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPLGKKLNVTAWKAQNPVLRVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAA**ATG**GAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

155/330

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRRLKLGQPTQHFWARL

155/330

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTTGGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTGCTCTA
 CCTCACGGCCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCACTCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCAATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACCTGTGGAACT
 CAACCTTGGCCCAACAATAACCTCTCTTCTTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGTGTGGCCGCTGTCTATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCTTCCAGTGCTCTGGCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGTTGCTGC
 TTTAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCAGCGCTGAGCTTAACACCTCCAACATACAGCTTCTTCAACACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACACGCGGAAAGTACAAGCCTGTTCCTA
 CCACGTCACCTGGTTACCAGCCGGCATATACCACCTCTACACACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACGTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCACAACAGCAGCTCCGTCGGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTC
 ATGACCATATTAACATACACACCTTACAAACCCAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGACACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGCCCA
 TACCAGGACAAGGTACAGGAACTCAAATA**TGA**CTCCCTCCCCCAAAAACTTATAAAAT
 GCAATAGAAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAAATTTAAAGA
 CAAAAAGTCAAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLKYLNLGMCNIKDMPNLTPLVGLEELEMSSGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDLW
LAWWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGvyTCMVTNVAGNSN
ASAYLNVSTAEINTSNYSFETTvtVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLPtiHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTTISEPYIIQTHTKDKVQETQI

CGCTCGGGCAGCAGCCGCGCAAGAGATGACGACTGGGTGCTGGACGCAAGTGGGGCTCACTTTCTTCAGCTCC
TTCTCATCTGCTCTGCCAGAGACATACAGTCAATTATGAAGCGTCTGCCCTGGAGCAGAGTGGGAATATCATG
TCTCGGGAGTGGCTGTAATATGATCAGATGAGTGGCTGTGCCCCGGAAAGAGGAAGTCTGGGATATACCATT
CCCTCTCTGCAGAGATGAGGAGAATGAGTGATCATCTGCTGATTCACCCAGAGTTGTACCACTTTTGAAGAACT
GCAAGAGCTGCCAAATGGCTCATGGGGGGGTACCTTGAGTGACTTTCTATGTGAGAGGGTGTCTACTGTGCAGAG
TSCCGAGCAGGCTGGTACGGAGAGAGCATGATCGGATGTGGCCAGGTTTCTGCAGGCCCCAAAGGTCAGATTTT
GTGTGGAAGAGCTTCCCTAAAGTACTGCTGTAATGACCATTATGCTAAACCTGGGTTTGTATCAACATATG
GATTTTGTGATCTTGAAGTCTGGAGTTTGACTACATGTGCGCAATATGACTATGTGAGTCTGTGATGGAGCAAC
CGCGATGGCCGAGATCATCAGACGGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATCCTCACT
CCACGCTCTCTTCACTCCGATGGTGCACAAGAAATTTTGAGCGTTTCCATGCGCTATTATGAGGAGATACAGCAT
GCTCTCATCTCCCTTTGTTTCCATGACGCCAGCTGGGTCTGTGACAAAGGCTGGAATCTTACAAGTGTGCTCGTGTG
GCGAGTCTCATCTGGGCGAGCTGTGAANAATCTCTTGGAGAAGAAAGACTGCTCAGACCTCGGGGCGCGATCAA
TGGGTATACAAAGAAATACAGGGGGCCCTGGGCTTATCAACGACGCGATCTCAAAATTTGGCACGGTGTGCTTCT
TATTTTGTACAACATCTCTATTTCTTATGTGGCAATGAGAAAGAACTGTCGACAGCTGGGAGAGAGTGGTCAGGG
AACACGGCCATCTGCATAAAGGCTGCGCAGAGAAACAAAGATTTTACAGCTGTGGAGAGGAGAGTCTTCCGAT
CGAGGTTGAGTCAGGAGGACACCATATAGACAGTACTATCCGCGCTCTCAGCAAGCAGAAATCCAGAGTGT
CCCCATCCAAAGGACAGGCCCTTCCCTTTGAGATGTGCCATGGGATACCAACATCTGATACATCCAGTCTCAG
TATGAGTGCATCTCAACCTTCTACGCGCGCTGGGACAGAGCAGGAGACATCTGTGAGGATGGGAGGTGGAAG
TGGGGGGCCACCATCTGTGATCCCTTATCTCGGGAAAGATTGAAGACATCACTGCTCAAAAGCACAAAGGTTGT
GCTCGGCTGTGCGACGGACCATCTACAGGAGGACAGCGGGGTGCATGACGCGAGCTTACAAAGGAGGAGCGTGG
TCTCTAGTCTCAGCGGTGCTGTGGTGAATGAGCGCATCTGGTGGTGGCTGCCACTGTGTACTGACTCGTGG
GAGGTCACCATGATCTAAGACAGCAGACTCGAAGATTTGTTTGGGAAAAATCTACCGGGATGATGCTGGATGTG
AGAGAGACATCCAGAGCTACAGATTTCTGTCTTATCTTGATGCAATTAATGACCCCATCTGTCTTGATGCT
GACATCGCCATCTTGAAGTCTCTAGACAAGGCGCGTATCAGACACCGAGTCAAGCCCATCTGCTGCTGCTGCGAC
TCGGGATCTCAGACATCTCTCCAGAGTCCCAACATCTGTCGCTGGCTGGAAATGCTCTGCGACAGTGAAGGA
CGCTTGGCTTCAAGAGACAGACATCTCGGCTCTGGGTGGTGCAGTGTGGTGGACTCGCTGTGTGTGAGGACAG
CATGAGGACATGGCATCCAGTGAAGTGTCACTGATGAATGATTTCTGTGCGAGTGGGAACCCATGCCCTTC
TGATATCTGCATCTCAGAGACAGGAGGACATCGGGCTGTGATCTCTCGGGGACAGCATCTCTCGTAGGCCACGT
GGCATCTGATGGGACTGGTCACTGGGACTGATGATAAAGATCATGAGCACAGGCTCTCACTGCTTACCAGAG
GTGCTGCTTTTAAAGACTGGATTGAAGAAATATGAATGACCAACTGCTCATGCACTCTGAGAAGTGTTC
TGATATCCGCTCTGACTGTTGTCTGATCGGTGAAGACGTGGGCGTGAAGTGTGATTTGGCTGTGAATCTG
CTGTGTCAGGCTCTGACTCTCAGGAGCAAAACTCAGTGAAGGTTGATGAGACTCAATCTGCTGTAGTGCATG
CGCGCTGCCACTATAGGACAGCAATTGGAAGATCGCAGGCTGTGCAAGAAAGTAACTTCTCAAGAAAGAC
ATATACAAAGCTCTCACTCACTGACCTGGTGGTCTTCCCAACTTTCAGTATTACGAATGCCATCAGCTGT
ACAGGAGGAGCTTGGGCTCTATGAGGCCCTTTTGAGGCTCTCAAGTTCTAGAGAGTGTGCTGTGGGACGCC
CAGGGCAGCAGAGTGGGATGTGGTGAATGCTTTTGTGATACGTGCCACAGTACAGTCTGTGCTCTTTCTTCC
CCTCTCTTGTACACTTTTAAATTAATTAAGTTTGGCTTCTGAACTACAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLREFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQVSRETPLH
QLYSAAFSKQKLQSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAATYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVVGKFYRDDDRDEKTIQSLQISAILHPNYDFILLD
ADIAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDVSLLEQEHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFTKVLFPFKDWIERNMK

ACACGGCATTGTATCTTCAGTTGTCTATCAAGTTTCGAAGTCAGATTGGAAAGCTCAACTGA
AGCTTTCTTGGCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC
TTCACCTGACTTTCCACCTTTCCCTACA AATTCGATTACTGTTGCTGTTGACTTTGTGCCT
GACAGTGGTGGGTGGGCCACAGTAAC TACTCTCGTGGTGCCATTCAAGAGATTCTTAAAG
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGAAGGGAAAACTGTGACT
AATGAAGCATCCAGGAAGAAGGTAGAACTTGACAAC TGTCTCTCTTACCTCAG
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
CCAAAGTGTCAGAGGGCCGGTATCGCCCTCAGGAATGTAAGCTTTTACAGAGGGTCGCCATC
CTCGTTCCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGT CATCCACCAGGCTGAAGGTA AAAAGT
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCAGCTGGGTACAGGTTACGTTACAGTG
GATATTTTGGGGGTGTACTGCCCTAAGCAGAGAGCACTTTTTC AAGGTGAATGAGATTCTCT
AACAACTACTCTGGGGATGGGGAGCGCAAGCAGTACCTCAGACTCAGGGTTGAGCTCCAAAG
AATGAAAATTTC CGGCCCTGCCTGAAGTGGGTAAATATACAAATGCTCTTCCACACTAGAG
ACAAAGGC AATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCAAGAGTCTGG
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATA
TATCAACATCACAGTGGGATTCTGGTTTGGTGCATGCA CCCTGGATCTTTTGGTGATGTTTGG
AAGAAGTGATTCTTTGTTTGAATAAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTCTTTTGTATTTTCTTAGCAGAGCT
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCGTGAGAGAACCAGAGTTGTTCT
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCTATTTATCCTGTACAATCATCT
GTGAAGTGGTGGTGTGAGGTGAGAAGCGCTCCACAAAAGAGGGGGAGAAAAGGCAGCAATCA
GGACACAGTGAAC TTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCCTCAGGGGAGGACCTGCCCAGGTATGCCT
TCCAGTAGTATGCCACAGAGATAACATCTCTATTAGTTTTTAAAGAGTTTGTGAAAATGA
TTTTGTACAAGTAGGATATGAATTACAGTTTACAAGTTTACATATTAACTAATAATAATA
TGCTCATCAAATACCTCTGTAGTAAATGTGAAAGTGAAGAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CTGTGGCCGGGGTCCGCAGCGGGCTGTGGGGCGCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTTCAGCTGATATCCCTCCGCGTCCGCGCCACGCTTCTCCCGCTCCGGGCCCGCCGAT**AG**
GCCAGGACGATGTGGTGGCGCTCGCGCGATCTCTGTGGTTGCTGCTCTGCCCTGGCG
CCCGCGAGGGGTGGCCCGAGGGCTGTGATGAATCAATCTCACCACCAGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGCGGACGCTGGTGGCCAAAGGACAACGGAGCCTGGGCCGT
CCCGCTGAGCCCACTTACCGCTTCCACTGGATCCACACCCCGCTGGTGGCTTACTGGCAA
GATGGAAGGGGTCTCAGCTCCACCATCGGTGTGGTGTGCCACAGCTGGCCGGGAATTCGCCG
TCTGTCTTGGGTCACTCCGCTGACTGTGGATGTGCCAGCCTGTGGCCAGGGGGTTTGT
GTCTTCCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTGACCCAGAACACTTCCCTTACC
TGTGGCCAGCTCTATCTACTAAGACCGCTGTGAAAGTCTCTCTTCTCTCCACGACCGGA
GCAACTTCTCAAGACCGCCTGTGTTCTCTACAGCTGGGACTTGGGGAGCGGACCCAGATG
GTGACTGAAGACTCCGCTGGTGCTATTAACTATTTCATCATCGGGACCTTCAACGTGAAGCT
CAAGTGGTGGCGGATGGGAAGAGGTGGAGCTGGATGCCAGGGGTGTGAAGCAGAGA
CCGGGGACTTCTCGCCTCGCTGAAGCTCAGGAAACCTTCGAGGATCCAAGTGTGGGG
CCCCACTTAATCAGACCTTCCAAAGATGACCGTGACCTGAACTTCTGGGAGGCCCTCC
TGTAGCTGTGTGCTGGCGTCTCAAGCTGAGTGCTGCCGTGGGAGAGGGGATGTCCACC
CTGTGTCGTGGCCAGCAGACGCTCAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
TGCTTCAGCATCCGGGCGGAGAATATCATCAGCAGAACATCATGATACCAAGATCCAGGT
GTGGCCCTCCAGATCAGCGCGGTGTCTTTGCTTTCCCATGTGCTACACTTACTAGCTGA
TGTTGGCCTTTCATCATGTACATGACCCCTGGGAATGCCATCAGCAAAGGACATGTGGAG
AACCCGAGGCCACCTCTGGGTGAGGTGCTGTGCCAGATGTGCTTGGGCCCTTTCTTGTG
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCCGGCTGTCCCGCCCCCT
ATAAGTCTGTCAAACCTTACACCGT**TCG**ACGACCTCCCCCTCCCCACCCATCTCAGTGTAA
CTAGCTGCTGACTTGGAGTTTCCAGAGGGTGTGTGCACTTACGACGAGGGGGTTCATT
TGCCTGGGGCTGTGTGCGCTGATATCTCCATCTGTACAGTTTCCGCCACTGCCACAAGCC
CTCCCTCTCTGTGACCCCTGACCCAGCCATTCACCATCTGTACAGTCCAGCCACTGACA
TAAGCCCATCGGTTACCAACCCCTTGACCCCTACCTTGAAGAGGCTTCTGTGCAAGCT
TTGATGCTTGGGGTGTCTCGGTGTGACTCTAGTGGGCGCTGGCTGCCCATGCCATGCCATTCCT
CTCATATTTGGCAGATCTGCTGTCATTGGGGGTCTCAGTTTCTCCCCAGACAGCCCTA
CTGTGCCAGAGACGTAGAAGAAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATGGGCACACTCAGAGAGAGAAGTGTGACTGTACACACACACACACACACACA
CACACACACAGAAATATAAACACTGCTCATGTGGCATTTAGATGATCAGCTGTGTA
TCTGGTTAAGTCGGTTGCTGGGATGACCCCTGCATAGACTGAAAGGAATTTGACCTCCA
AGAGCCCTGACAGGTTCTGGGCGCGGGCCCTCCCTTTGTGCTTGTCTGTGAGTTCTTGC
GCCCTTTATAAGGCCATCCTAGTCCCTGTGGCTGGCAGGGGCGTTGGATGGGGGGCAGGACT
AAACTGAGTGATTGCAGAGTGCTTTATAAATACACTTATTTTATCGAAACCCATCTGTG
AATCTTTCATCGAGGAAAGGCCCTTGACGCGGTAGAAGGTTGATCAGAGCCGGGCGCG
TGGCTCAGCCGCTGTAATCCAGCATTTTGGGAGGCCGAGGCGGGTGGATCAGGATCAGGA
GATCAGAGACCCTTGCTTAACACCGGTGAACCCCGTCTCTACTAAAAAATACAAAAGTT
AGCCGGGCGTGTGGTGGGTGCTGTAGTCCAGCTACTCGGAGGACTGAGGACGAGGAATG
GTGCGAAACCCGGGAGGCGGAGCTTGACAGTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
GTGACAGAGCGAGACTGTGCTTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEEPDATTRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLFLGSPPLTVCWRLKFECLPLEEGECHFPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGCGAGACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCTCCCTTCTTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCCTTTGTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT

THE FUTURE OF THE PAPER

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKKT

FIGURE 166

CTGTCAAGGACCACCTCTGAAGGCTGCAATTTGTTCTTAGGGAGGCGAGTGCTGGCCTGGC
 CTGGATCTTCCACCA**ATG**TTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTTCAACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCACTTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCCTGGAACCTGCTGAGCAGAACCAATTATAAATTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGTCTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTCGGTGCG
 AGCGCTGACAGCCATCATCACCTACCATTGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCAGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCCTG
 CCCACACGCTCTGGTTTGAAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAGCAAGCTGCCTATCTCATCTTCCCAGAAGGAACCTGTCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGGAAGTTTGAATTGGAGCCACAGTTTATCCC
 TGTTGCTATCAAGTATGACCCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGACGCTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGGCAATAGGGTGAATCTGCG
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACCTGCTGTGCTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTGCCCCAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTTGTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAATCCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGGCCACCCG
 CTCTCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCTGCCCCAGC
 CTTGGAGCTCTGCGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAAGAAATG
 AAGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCCTGAATCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTGGGGG
 GAATGGTGGTGATTTCTTACCCTACAGGGCTGTGTGGGGATTAAAGTGTCTGCGGGTGAAGTA
 AGGACACATCACGTTTCAAGTGTTCAGTACAGGCCACAAACGGGGCAGCGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSTFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLLEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAELESWNLLSRTNYNFQYISLRLTVLWGLGVLI RYCFLPLRLAFTG
ISLLVVGTTVVGYLENGRFEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCC GCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGATGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCITCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGAGAAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAACTCTGAGGGGGCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCAGCTCTCAGGGGTGGGCCCTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAAG
ATGTTGGCCTGGGGAGGCCACAGCAGGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVF RVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTL LLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCAGAGAGCAAT**ATG**GCTGGTTCCTCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTC
TATTGCTCTGGACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACAAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTFLVT
IQPEGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCCLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTCAACATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGTCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCTCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGTTTCT
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTTCGGGAA
ACTCCTAACATATGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAATCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCTTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAGAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAA
TTTTCATGAAATTATTCCTCTTCTGTTCATAAATGATTACCTTGCACTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

FIGURE 176

MTCCGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTGGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

Figure 1

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

[illegible]

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
 YKSSQKQHSVPVEKAIPITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTGCTGCTGAGCCTGCC
 TGCGTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCTCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAACCTGGTTTGGGGTCACTGGGCCTGATCACTCTC
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCACTCCGGGAGCGGCGTGG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGCGCAGTGGCCTCTC
 CTGGGTCTCTGTACAACCTTGCAGGGCACCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCCAGGAAGTGCATCGGGCAGGCGTTTCGCATGCGCGAGATGAAAGTGGTCTGG
 CGTTGATGCTGCTGCACTTCGGTTCTTCCAGACACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCA
 GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTGATGAATAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKFWLGEGLLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDIFDVLLLSKDEDEG
KALSDDEDIRAEADTFMFGGHDTTASGLSWVLYNLAHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCCTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCTTAACCTCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACACCCCTGTTTATTGTTACCTGGAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGTCCGACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCTGTTCCTGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCCTAAGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCTGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAAGTGAATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTACA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTTCTAACAATGAAATATATTACAGGCAGGTACCCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACAAGA
 GCCTCCTTGTTTATAACACAGGTTACCCTACAAACCACTGTCCCAACACACCCCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACGTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW
VVRAAHLTPLEYVNPPEPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRFAGVVPGA

188/330

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TCCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTACTGGAACCTGCCTGTGGGCTCAAAGTACAGCGCCTTTGCTG
 CTGTTTCCTCTGTCCTGTCAAGTCTCCTGGGGATGGTGGCCACATGATGTATTCACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGGAATTATGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTACCTGCTGCATGGCGTCGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCTCGGGGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACAGCTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTCACCCAC
 CCCACATCTCACACATCCGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEYVQYNWETGDDRFSEFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPGCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSDCQLGSRRLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

190/330-190/330

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCAG~~ATG~~TGGTTACCCCTTGGTCTCCTG
TCTTTATGTCCTTTCTCCTCTTCCTATTCTGTGTCATCTCCCTCACCTTAAGTCTCAGGCCTGTCA
GCAGTCCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCTTATCCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTGAG
GACATTCGCCCCCTGTGTGCCACCAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGCTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCCTGCTGAATAATCAAGTGGGAGGGGAAGCA
GAGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACAAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATCTGATTCCAAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 192

MWLPLGLLSLCLSPILSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

192/330

GTAGCGGCTCTTGGGCTCTCCGGCTGCGCGTGTGCGCGCGCGCGCTCGGGTCGTGGAGCCAGGACGACGTCTA
CGCGC**ATG**TCGAGGAGTCAAAAGCTTTGATTAGTTTGTCTTGTGGAGGAGCAATTCGAGTGTGTTTGTATGCTT
GGATGTGCCCTTCCAAATACACAAACAACTAGCCCTCTTTGTTCTATTTTTACATCTCTTACCATTCC
ATACTCATGACAGAAAGGATGATGGATGATACAGATGCTATGATGAACGCTTTGAAAGCAATTCGCATCTTC
TTACAAACGGGATCGTGTGCTGACGTTTGGAGTCCCTATTGTATTGGTCAGAGACATCTGATTGAGTGGGA
CGTTGTGCACTTTGTCTACAGGAAACAGACATCACTTGAACATACTATAGGCTTTTCTTGCTCTTTGGAA
CAATGACGACTTCAGTGGCGGACGATGGT**AGT**AAAGAAATCTAGCAACTTGTCCAAATGGACTTCGCTGATCT
TTGTGCCATCTCAGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGAACGCTCTTGGGGGATTTTA
GGTGCCTCCCTCTCACTTTTATTGTAACTACTATTTCACAGAGACTGCTGAGGAGTAAAGAGATTCTCT
CTTTTGGAAAGGCTTGACTGATTCTACACATTATCTATAGTATGCTTTGTGGTGCCTCGAATTAATAAT
TTATGTGTTTCTGCTTGATTGTTTATTTTGGAACTCAATGCAATGTAAACACTTTTAAATGATCACTA
TTTGTCATGGTTAGGAAATCGAAATTCGCGCGGCTCTATTACGTGTCAGTCACTCTTTCTTAAATATT
TAGCCTTCATTTATACAAAAATATAAAAATAGTTTTCAGTCACTGAGTACATCACTCCCAATGTTATG
CAGACATACAGACGGTTGGCATCTGCTATAGACTGTATCACTCAGTGCAAATATAGCTGCATTTATCACTCAG
GGCGAAGTGTGATGCCATGCCCTCCGTTAAGGGTGGTGGTTTCTCTGTTAGAGACAGATGTTTGTGGATT
AAATATTATTATGAATTGCTACAGAGGAGTCTTTCTCTCTCAATTTGTAGAAGATTTATGTAAACCTTA
AGGTAGGGTGTAAACAACTTTTGAATAGGTTTATTTATGTGTTATTAATGTGTAGAGTGGTGTCAAGT
GGGAAGAAATGACATTGAATTCAGTTTGTGAATCTGTTCTATTTTAATGAGAAATGTGATCTCCATAT
ACCTTCTCATGTTTACCGTTTAAATGGACATCACTGGAACCACTAGTGAGGGACAGTTGTATGTGTC
ATCATATATGCGGAAAGACCTTCCTCTGCTCTCTTTGACTTATTTGGTATGTTGATATATACATAAAA
TAACCTTTCAAATATAGTTTAAATACACTAGAAGTGTTCATCTACCTGAAATAAATGCTATCGCGTACAT
CAGAGTGGCCCCCTCCCTCGCAAGGCTCTGCCATGATTACCAAGTACATGTAGTCTACAGATTAATCAAGCA
TTACAGTTTAAGATTAGACCATGGTATAGTAGTTCTTATCTCTAAGTATATATCATGTAAATTAAGG
TTTTTTAAGACGATTTCTCTGTGATCTCTGAACTGTTTGATTTTGTAGTCATCATATAGTCTGTGTTT
CCTTATAAAGCAATTTGTGTGTGAGTTAATCAAAGTAGCAAGTCCAGTATATAGACGCTTCAGAAACA
ACCTGACCAAAAAATCCCGATACACCGGATCAATTAATTTAGATGGTCTTTTACATCATATAATTTACAGCA
CTTTTTCAGGATGGGTTTAAAAAACTCAAGTTGGTCTGACAGTATTTGTGAAGATTTTGTGTATG
TTTTATCAGTATCTTACATAAAAAATTTCTCGCATCAGCCAAAATCAGTAATCATCAGACGCTGTCTGTGT
TTTTAGAGTTTATTTCTCAAGAAAAATGGGAATAAATTTGGGATTTGTCACTTTTTATTAAGATTGCTAA
AGCACAGGTTTATTGTGCTCACTTAAGCCATGACTTTAGATATGAGTAGCGGGAAGCAGGACGAAATCG
CGCTGTGGCTGGAGCGTCCCATCGAGCTGGAAGTGCCTGTGGTATTATTAATGTTCAGATTCTAAGAGAA
GGTGCAGGTACACATGAGTTAGAGACGCTGTGACAGACTTGGGAAGTCTTGTGCTTGTGATCTAGTGAATCT
TTTTTTCAGGAAGTGTCATTTCTCTGCTCTCCCTATTCTTCTGCTCGAGTCACTGAGCTGACTGCTAGT
TTTTATCCACTTGGCCACAGACTTTTCTACAGCTCGGTATTCTTATATATACTAATGTAGTTGGCAGCAT
GTGTCCTGACCTTGTATACGTCTGTACATAGTGTCTCTGATTTTAGGCTAGTTCATGATATGAAT
TTCCTCATGAAATATGCATCATACACATTAACCATCTCTCTATGGAAAGAACTTTGATGATGAACAAATAA
AGATTTTAAATATCTTTTAAAAAAAAAA

CCACAGCGCTTCGCCCGACGGTTCGCCCGACAGCTTCGCCCGACAGCGTCCGCACAGCGCTCCGCC
CCAGCGTCCGGTGCAAGCTGCTCCGCGACACTGCTGCTGAGGGAAGACAGCCGGCGGCTCTCCGGCTCGT
CTCTCAGCTTCGCCGGGGGCGCGAATGGCAGCTGTTTCCGGCGGATAAAAGTCCGAGCGGTCAGTGGTCTGTTT
CAATCAGCCAGCAATTAAACAGCATCTGCAGATCTCTGGGGATGCGCAGCCCGAGTTTGGAGTTTTCCTCCCAAC
AAGCTCACAGTCCGAATCGCAGAGGAAAGGAAGCGGAGGAGGAGGACGCTGGGGCTCCGGCAGCATTTGTTG
GAAACTTCGGGTTCTAGAAGTTCGCTCTCCCGCTTCGGCGCGCCCTTCGACCGCCGAGCGAGCAGCAAGT
GAGACATTTGGGCTTCGCATGTCGCGAGTTCGCGCGCGGAGTTCGCGCGCGGAGTTCGCGCGCGGAGTTC
GCGTTCGATATAAGTTCGATCAAAAGCGGAGTTCGATGAGGAGTTCGCTACTCTCGAAAGGAATTTCTC
CTCTCTCTAGTCTGCTGCTGAGGAGGCCCTCGGGGTTGTTGTGTGTCGTGGGCTGCTTTCAGATCGT
GCCCGCGCCCGCCCGGGGTCGCCCGACCTGTGCCGTGTCGCGGCGGGCTGTCTGATCGGAGGCGCTCAAC
CCACGAGGCGCCCAACAACCTGCTCGCGCTGCTGGGCTTGTGCTCGTACAAACAGCTCTCGGAGCTGGC
CGCGGCGATTCACAGGGGTTAATCGAGCTCAGCTGGCTCTATCTGGATCAACATCAATCTCTCTGTCGAG
GGACGCTTTCAGAAATCTGCGCGACTTGAAGCAATCAGCTGAGTCTGCGCGCGGAGTTCGCGCGCGGAG
CAACATCTCTGATGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAG
CTCTCTCAGCTGCGCGAGCTCAGTTCGATCGATCGATCAATCAGTCAAGATCTGGCGCGCGCTCTT
TCGCGCGGTTTCTTAAGCTCAGCGAGTCTGCGCTGCGGAGCAACAGCTTGTCAAGTGTGATCTCGCCACTTC
CGCGCTCATCTCCTCGACTCTGCTGCTCGCGGAGCAACAGGTTGGCAATTTGTCAGTCTGCGTGAAGT
GGTTTGGAACTCTGGAAATATGGACTCTCGGCGACAGGATCGAGTCACTGCGCGGAGTTCGCGCGGAGT
TCGCCAGCTCTGAGTCTGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGT
CTCTCTCAGCTGCGCGAGCTCAGTTCGATCGATCGATCAATCAGTCAAGATCTGGCGCGCGCTCTT
CTCAGCAACTCTCAGGGGCTCAGATGGCACTTCGATGCGCGAGCCGCGGAGTACGCACAGGCGAGGAGCG
TCTCGAGCGCGGTGTAGCCTTCCACTGTGCGAGGATGGGCGAGCCACAGCGCGCCTGCTCTCGCG
CTCAACACCGCAGTGTCTGGGGCGGCTCGACAGTTCGGCCACACAGCTCGCGGAGCGGGGAGGGGCGCA
CGAGCGGCAATCTGAGGCTGCGACCGTGGCTTCTCAGCGCGCGGAGCAACGCGGAGACCTCTCGACAGT
AGGTGTCACGCGGCAACAGCTGGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCG
CATCATCTGATGGCTGCCATCTCTGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCG
TGTGTATCATCAAGCATGTGGTCTGCTTACTTCCAGCAGGACCGCGCGGAGGAAATCGAGGTTGAGTATCC
CAGTGGCTTCAACCACTGGCTCGGATACGCTTGGCGCGCGGAGCGGCGCGGCGCGAGCGGCTGGGT
CTCTGTCTCTGCTCTGATATCTGCTTGTACTGAACTTTAAGGGTCTCTCCACAGAGCTTCAGATTTGAT
TTTATTTGTCTCTTAAAGCAAGGCGAATTAACACATCAAAAGAAATCTCTCCACAGTTCAGATTTGAT
TATCTGATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTCTGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGT
AACATCATGATCTAGAAGTCTTAAGTCCATAGCATTTCATGAGAACCTTCAAAGAGGAATCTGCAATC
TGGGAGGCTTAAGAGCAAGATGACCATCAAGAAAGCTATGTTCTACTTTTGTGTGTGTCTGTATGTTCTCGG
TTGTGTCTCTTTGTAGGCAAGCAAACTGTTCTACAAACAGGGAATTTAGTCTCAACATCTTTCAGCGCGT
GCCTCTAGCTCTTGGAGTTTGGTGGGGGGAGTGGGGGGAACCGCGAGGAATAGGGGAAGTGTGATTTG
AAGTTTGTGATCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTCTGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGTTCGCGCGGAGT
CCACAGAGGCTCTAATCTATTACTGCTGCTATCGAAAGAACTTTAAGGCCAATTTCACTCTCTGCTCTG
GGCATTTGTATGGATTTGACCTCTGTTTGCAGTCACTTCCAGCTGATTAAGTTCAGAGTGTGATTTAGGTT
TTTGGAAATTTTATAGAAAAAAGTCTTTTCATGTACAATGACATCTCACACAGTCTTAGGCCCTAGTAT
GTTTTTTAGTTTGGACAGGAGGAAGGTTTAAATGAGCTGCTCTCTGCTCACTCGAAAAATAGGACAG
CCCTGTATCTAGCTCTTGGCTTGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTCTGAGCTCATCAAGATGAGAAGGCCCAACCTTTCTCTCGCTTCBAGAAGGCGACATTTGGTATG
ATTTAGCATCAACACATTTATGATATATATGATATATGATGATCAGAGGGGCAATGCCACTTGTATTTCTCCCA
AGTTTTCCAGAAGATACACAGATCTCTGATAGGATAGGCGGCTGTGTTTTCGGGTTTATTTAGTGA
CTGTGACAGAACTTTGATGCTAGTCTATCTGACATGGCCAGTAGACAGGCAATGTGATGATCATCAGAG
GAGTAGAGAACTCATCATCACTACCTCTCACAGAGAAATTTGATGATGATGATGATGATGATGATGATGAT
AGCAAGATGATGCTCTGCAATCAGAGATCTCAATAAAAGCAATAGCTAGAATATGACCATTAATGTGCTT
CGAAATGATTTTGAAGATGGTTTGAATGTCA

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDAPQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGCGTTCAGTTCCCGCGGACAAGATGG
TGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCCTGGCGTCCGCGCGGGCCGCCTACGCTTCACGGGCCGGGCGCGCT**TGA**GCGTG
GGCCCCGAGGACTGCGCGGACCCGTCCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVS DM L L P L D G E L V L A S G A G F G V S D V G S H L D C G A G E P A V F R D S D R F S W H D P H L W R S G D E A
P G L F F V D A E R V P C R H D D V F F P P S A S F R V G L G P G A S P V R V R S I S A L G R T F T R D E D L A V F L A S R
A G R L R F H G P G A L S V G P E D C A D P S G C V C G N A E Q P W I C A A L L Q P

[illegible]

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGGTTCCCTCCAGTCACCCCTCCCGCGGTTACCCGCGGGCGGCG
 CCGAGGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATAGTACTTCGAATTTATCTTTGGTGTCCCTCATACTTGCTGCAGTGAAGTCTTTC
 AACCCACTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGTATGGATTCCGTTGGGATTACT
 TATATAAGGTTCCAAAGCGCCCAITTTTCAITATATTATGAAATATGGTTCACGTTGAAGCAAGTTACTAATGTT
 TTTATTACAAAAACCTACCTTAACCAATTATCTTTGGTAACTGGCCTCTTTCGAGAGAATCATGGGATTGTTGC
 AAATGATATGTTTGTATCCTATTCCGAACCAATCTTTCTCCTTGGATCACATGAATTTATGATTCACAGTTT
 GGGAGGAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATAGTGTGTCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCTACTCATTACATGGCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCACTACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGTTAAATTTGATGAAGTCTATGAAGCACTAATCAGCT
 CATCTTAATCTTACTGTTTACAAAAAGAGAGCTTCAGAAAGGTGGCATTACAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTAGTGTTAAACAGCAGAATATGACCAAGAGGGGTATACCCCTTATTTTATAGGGGTC
 TCCTTGGCAGCATTATAGTGATTGTTTTTTGTAAATTTTCAATAGCATTAAATTCAGATCAAAATACCTGC
 CTTACAAGATATGCATGCTGAATAGCTCAACCAATATTACAAGCCTAAATGTTACTTTGAAGTGGATTGCGATA
 TTGAAGCTGGAGATTCCATTAATTTATGTCAGTGTTTAAAGGTTTCAAATCTGGGAAACCAGTTCCAAACATCTGC
 AGAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACACACAGGCCAAAA
 ATACTTACACCTGCAAGGAATAAAGATGTAGAGATATGCTCCATTTGTTCACTGTAGCATAGGGATAGATAG
 ATCCTGCTTTATTTGCACTTTGGCCAGATAATGTATATTTAGCAACTTTGCACTATGATAAGTACCTTTATAT
 ATTGCCATTTAAATTTCTCTCCTGATGGTACTTTAATTTGAATGCACCTTTATGGACAGTTATGTCTTATAAC
 TTGATTGAAATGACAACTTTTGCACCCATGTACAGAATACTGTTACGCATTGTTCAAACCTGAGGAAATTT
 TCTAATAATCCGAAATGATGAACATAGAATCTATCTCCATAAATTGAGAGAAGAAGGTGATAAGTGTTGA
 AAATTAATGTCATAACCTTTGAACCTTGAATTTTGGAGATGTATTTCCCAACAGCAGAAATGCAACTGTGGGAT
 TTCTTGCTTATTTTCTCCAGAACAGCTGGTTTTCATTATTTTCCCTCAAAGAGAGTCAATACTGACAG
 TATCGTTCAATATATTTCTGTCATAAAATTAATGTGATTTCTGATGAGTCATATTTACTGTGATTTTCA
 TAATAATGAAGACACATGAATATACTTTTCTCTATATAGTTACGCAATGGCCTGAATAGAGCAACAGGCA
 CCATCTCAGCAATGTTTTCTCTGTTGTAATTTGCTCCTTTGAAATTAATCACTATTAAATACATTAA
 AAATCAATTTGGATAAAAA

FIGURE 202

MTSKFILVSFILAALSSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQIRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTNLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTELDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHELLNITAMPHNGSFWNVQDLNLSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCCAG
 GACAGGCCCCACCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTTGCTTGGGTACACAGCCAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCAACCAGGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCGTGACGTTGCC
 CCTGCCCCTGCCCCCGACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCGTGCTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTGAGAACGGCAACTCTTAAGGTTAAAAACAGATGAATGTACAATGGCCGCCA
 AGATTCAACACCTTGAGTTGAGTGTCTGAGAAGCCCCCTGGACTGATGAGTTTGTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTGAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALLVLAEILIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTTSLSRSMPPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
220

GGGCTCGAGCTCGAGTGAATCGGCTCGAGGCGCAGTGGAGCACCAGCAACCGGCCAACTT
GCTCTGTCTGTGCTCTACGTCGCGGCTCGCTGGGGAAGCCAGACAGGATCTTCAGTACTT
 AGTGAAGCTGGGCTCCCTCGGCGAGTGAAGTCCATTTCAAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCTCCACTCCCGCAGTGAAGCAGAAAAATGTACAAGCTGGAGATAAGCACT
 TGAATGGGCAGCTAGACTTTGAAGAAATTTGTGATTTCTCAAGTCTATGAGAAGAAGCTGA
 GGCCTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGATTGACGCGCAGGAGATCATG
 CAGTCTCGCTGGCGGACTTGGGAGTCAAGATATGTGAACGACGAGCGAGAGACTACCCTCTCC
 CATGGATAAAAAACGGCAGCATGATCAGTCTGCAATGAAACAGTGGAGAGACTACCCTCTCC
 ACCCGCTGGAAAAACATCCCGAGATCATCTCTACTGGAGAGCTTCTCAAGTCTTTGATGTG
 GGTGAGAATCTTAACGCTCCCGGATGAGTTCACAGTGGAGGAGAGGCGACAGGGGATGTGTG
 GAGACACCTTGGTGGCAGGAGGTGGGGCAGGGGCCGATACAGAACTCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGTCTATGCGAGGTCCATGCTCGCCGACACCAACATGGGCATCTGTGT
 GGTCTTCACTCAGATGATTCAGAAGGAGGGGCCAGGTCATCTCTAGCGCGGGCATGGCATCAA
 CGTCTCTCAAATTTGCCCCGAATCAGCAGATCAAATTTCACTGTCTATGGCAGCATAGAGGCC
 TTGTTGTGATGACCAAGGAGACTTCGAGGATTCAGAGAGGCTGTGTGCGAGGGTCTCTGGCA
 GGGGCGATCGCCCGAGAGCGGCTCTCCAAATGGAGCTCTGAAAGCCCGATGGCCTCGCG
 GAAGACAGGCGCACTACTCAGGAATGCTGGAGTCGCGAGGAGGATCTCGCCACAGAGAGGGG
 TGGCCGCTCTTCAACAAGGCTATGTCGCCACATGCTGGGAGTCTCCCTCTCGCGCATG
 GACCTTTCAGTCTTAGAGAGCTCTCAAGAATGCTGGCGCAGCATATTCAGTGAACACAGCTG
 GGACCCCGGCGGTGTGTTGCTCTGGCTCTGTGCACATCTCACTAGCTCTGGCCAGCTGGC
 CCAGCTACCCCTGGGCTTAGTAGAGCGGGGCTCAATATCCCGCAGGCTCTTATTAGGGCGCT
 CCGGAGGGTGACCATGAGCAGCTCTTAATCAATATCCCGCGGACGAGGGGCCCTCGGCT
 GTACAGGGGGCTGGCCCAACTCATCAAGTCTATCCAGCTCTGACATCAGCTACGCTACGCTG
 TCTACAGGAACCTGAAGATCACCTGGGCGTGCAGTCCGGCG**TGA**GGGGGAGGGCCGCCG
 CGAGTGGACTCGCTGATCTCTGGGCGCAGCTCGGGTGTGAGGCATCTCAATTTCTGATGT
 TGCCACACATCTAGCTGTCTCGAGCAGCTCTTGAAACCTCTGACACACCGCAGGAGGCT
 GGGGAGAGCTGGCAGGCGTAGGCTGTCTGACAGGCTGACAGCAGAGCCCTCTCTGTGTTGT
 AGCGAGAGCTCAGGATTTCTGAGCTCTGCGCAAGGTGAGCAGCTCCGGGCTCAATGTGTAA
 GGACAGGACATTTTCTGAGCTCTGCGCAAGGTGAGCAGCTTTGGAGCCTGGAGCCGGCTTACT
 TCTCATCAATTTCTGAGCAGCTGTTGGCCAGGCCCTGCCCTGTGTCTCGCGCTG
 ATCTCATCTGCGCTCTGTGCTGCGCTGCTGTCTGTGAGTAAAGTGGGAGAGGGCTACAG
 CCTCATCCACCCCTGCTCAATCCCATATCATATGAAGAAGTGAGTCACTGTGCCCT
 CCGAGGCCCTGACTTCCCAAGCTACAGATTCACGCCAATTTGGCTGTGAAGGAAGGAAAG
 GATCTPGGCTTGTGGTCACTGTCATCTGAGCCTGCTGATGGCTGGGGCTCTPGGCTAGCT
 TGGGACTCGAGCTGGGCTCGGCTCTGCTGCGCTGGCTGCACAGAGGCAAGTCTGGGCTCA
 TGGTCTCTGAGCTGGCTTGACCTTGACCTGTCCAGTGGGCCCTCAGAACCAAACTCACTG
 TCCCCTCTGTTGACCTGAGGCAAGTGAACATGTTGAGGGCGAAGGGCAGCGCTTGTGT
 GTGTTCTGGGAGGGAAGGAAAGGTTGTGAGAGCTTAATATGCAATGTTGGGAAAGGG
 TTTTGTCCAGAAGGCAACCGGCACAATGAGCGACTTGTGTCTCCAGAGGAAGCAGGG
 GAGCAGGAGTCTGGCTGACTGCTCAGACTGTGTTCTGACGCCCTGGGGGTTCTGTCCAAC
 CCAGCAGGGGCGACGGGGACAGCCCAACTTCCACTTGTGTCACTGCTTGAACATTAATTT
 ATTTTCTAATTTATTTGAACAGAGTTATGTCTTAACATATTTATAGATTTGTTTAATTAAT
 CGTTGTCAATTTCAAAGTTTATTTTTTATCATATTTATGTTCTATGTTGATGTACCTTCC
 AAGCCGCCCAAGCTGGGATGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTGCAGTACAT
 CTGCTCCAGAAGAAATTTCTTTTGGGACTGGAGCAGAAAGCGGGCAGAGGACAGCCGCTGT
 GCTCTTTCTCTTGGCAGGTTGGGAAAGGGCTTGCCCAAGCTTAGATTTAGGTTAGGTTGA
 CTGGGGGCTGGAGAGAGAGGAGGAACCTCAATAAATCTTGAAGTGGAACTCAGTTTATTTCT
 CTGGCTCGGAGGGTTCTTTAATTTCACTCTTCTGTTGAATGTCAAGGCATGAGTGGCTCT
 CACTCTGAATTTGTGTTGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCGCTCCCTCC
 CAGCCTTCTGCTGGCTTGTCTTAACATCGCGGCAACTGGCAGCTACGGTGTGACTTCC
 ATTCCACCAAGATGACCTGATGAGGAATATCTCAATAGCAATGAAGAATCAATGCAAAATTT
 GTTATATATGAACATATACTGGAGTCTCAAAAGCAATTAAGAAGAATTTGGACGTTAG
 AAGTTGTCAATTTAAGCAGCCTTCTAATAAAGTTGTTTCAAGCTGAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 206

MLCICLYVPVIGEATQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKLK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIAIKFMAYEQIKRLVGSDDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPMNLGIIIPYAGIDLAVYETLKNWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAASIEGAPEVTMSSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAAACAGGGATCTACAGAATATTTACACCACAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTACACAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCACTCGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

MASLGQILFWSIIISIIIIILAGAIALIIITGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSBQDEMFRGRGTAVFADQVIVGNASRLRKNVQLTD
AGTYKCYIIITSKGKGANLANLEYKTGAFSMVNVVDYNASSETLRCEAPRWFPPQPTVVWASQVD
QGANFSEVSNSTFELNSEVNTMKVSVSLVNTINNYSYSCIENDIKATGDIKVTSEIEKRR
SHLQKLLNKSASLVCSSSFAISWALLPLSPYLMLK

FIGURE 209

[illegible]

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

210/330

FIGURE 211

CTTCTGTAGGACAGTCCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGAAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTGAGTAAGCCACCTGTCTGCTGCTGGTGAAACAAGACTCTTGGAGGAGTCA
 TCTTTGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCGTGACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTTGAAGGTCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAAGTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTTATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 213

GGCCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCTCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTCTGCTGCTGAATCTGGGTCCCGGGCGGGGGGCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTACCCCTCACCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSSAINEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTFPPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

CGGGGTGCAGCCACCGCGCGGGGAGAGGAGTGGCGCGCGGTGGTCTGCTCTGACTGGGGCA
CCGGGCTGGCGAGCGCTCCAGGCGCAAGCTGAGCGGCTGACCGCATGCGTATGTCAGTGCAGAGAAC
GAATCTCTTGGGGGCGCTCTGAATCACTTCGGCTCCGGCCAGCAATCTACATGACTTACGACGCTGGAAC
CTCGGACACTATGAATGATGAGTGATGTGGCTTACCGTTGGCTCTACCTCAGGAAGTACAAAGTGCTC
CACTTCATGTCACAGTGGCCCTTCTCCGGTTCCTGTCTTTCAAGAGCGGCACTGGCCGTGGCTCTGTTCT
CAATGGCTGGCCAGCTGGTGATGCTTCGCCCTACCGCACTTCGTGGCAGCCTCTCCCCACTGTACCA
CTGTGTGGCTCTGGCTGGGTGTGCTTCAATGATGTTTGTGTCACAGTCTTCCACACAGGAGCATGT
CTGCACAGAGAAATGGACTATCTGTGCTGCTCACTCATCTCACTCAATCTACCTGTGCTGCTGACGAGC
CTGGGGCTCGAGCAACCGACTGTGTCAGTGCCTTCGGGGCTCTCTGCTGTCTAGCTGACCGTGCAGCTCT
CTTCACTGAGCTCACTCCGCTTCGACTATGGCTACAACCTGGTGCCAACTGGCTTGGCTGTGTCAACGTT
GTGTGGTGGCTGGCTGGTGTGCTGTGAACACGGCGGGCTGCTCAGTGGCAGTGGCTGGTGGTGGTCTT
GCTGTGTGCAAGGGGTGTCTCTCTCGTGCAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGATGCTGCA
TGTGGACATCAGACCATCCGTGTCCAGTCTGTTTTCAGCTTCTGAAGATGACAGCTTCACTGCTGT
AAGAAATCAGAGGACAAGTTCAAGCTGACAGAACATTTGAGCGAGTCTGCCCAAGTGGGATCTGCCCC
GCCCTTGGCTCCCTTCTCCCTCAACCTTGAAGATTTTCTTATTTCAACTTTTGAATTTGACATTTGACAT
AGGATGTGGGGCCAGAATGACTGTGGCCAGGCCACCCCTGTTGGCCCTCACCACAGCTTGGATGTGTTTGA
AAGCCCTCCAGGATCTGGAGCTCAGAGTGGGACGCCCTTCACTCTTGGAGCTGAATGGGTGGAACTGAC
GTGTGTGTTTGAAGTCTACGGGAGGACAGAGTGCCTGTTTCTCCCCACAGCTCTCTCCCAATCTCCCAAGT
CTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACAGGGAACAGCCCTTAGGATACAGGGGGTCCC
CTCTCTGTACACACCCGCCCTCTCTCAGGACAACACTAGTGTTGTGCTGGATGTGTGTTCTTTCGCGACCA
GGTTACGGGCGATTTCCCATGGATTTGAGGAGCAAGCTCTGGGATGGGAAGGATTTCACTTCACTTGA
GTGTTCTTGAAGCGTTCCAGAGAGGCTTCAACATCTCCCTTTCAGGGCCAGGCTCAGCAAGCCCAAGGGCA
AGATCTCTGTGCTGTGTTGTGTTGAGAGCTGCCAAGTGTTGCGGAGTGTGGCCAGGCTGAGTGCATGAG
TGACAGGGCGCTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCACTGTGGAGACGGGTGTGT
CGGGAGAGAGTGTGGCTTCAAAGTGTGTGTGTGACAGGGGTGGGTGTGTAGCTGTGGTATAGGGAACGTGT
TGCGGTGCTGTGGGCTGTGAGATGAGTGAAGTGGCCGTGAAATGTGCACAGTTGAGAGGTTGGAGCAGAT
GAGGGAATCTGTGCACATCAATTAATCACTTGTGGAGCGCACTTGCCACAGACGCACCTGGGCGGACAGC
CAGGAGCTCTCCATGGCCAGCTGCTGTGTGATGTTCCCTGTGTGGTGGCTTGTGCCCGCTTGTGCCCGCT
CTACAGGGTCCCAACACACAGTGGCTTCCAGAGCAGCCCTCGGAGGACAGGAAGGAAATGGGATGGC
TGGGGCTCTCTCCATCTCTCTTCTCTCTGCTTCGATGGTGGTCTTCCCTCCCAAACCTCCATTCCTCC
GCTCGACGGCTTTCGATAGGCTTGTGTTGGGAGGAGGAGGGCGCATTTAGGGAAGAAGGGAAGAACT
TATGGCTGGGTGTGTTTCTCTCTCCAGAGGCTTACTGTTCTCAGGTTGGCCCGAGGCGAGGGGCG
ACACTAGCTGCTGCTGGTGAAGTGAAGTGAAGCTGCAATTTACACAGACCTGGCATTTCTGCCCCACG
AATAGAAGTGAAGGAGCTCGAAACTTTTCATCCCAAGGACAGTCTCGCTGGTTGAAGCAGACTGGATTTTG
CTCTGCCCTGACCCCTTGTCCCTTTTGGGAGGGGAGCTATGTAGGACTCAACCTCAGGAGCTGGGTG
GCTCGCTGACTGTTTGTATACTGAAACTTTTAAAGTGGGAGGTTGCAAGGAGTGTGCTTAATTAATCAA
TTCAAAGCTCAAAAATAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPEKSSSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGQLQVINGLNSTEPVKEYAAF
 VLGAAFSSNPVKQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPKQLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELGGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTGCCTTGCCACCCCCA
 CGCGGACTTCCCAGCTTGGCGCGCCCCCTCCCATTTGCCCTGTCCTGGTCAGGCCCCACCCCC
 TTCCACCTGACCAGCC**ATGGGGG**GCTGCGGTGTTTTTCGGCTGCACCTTTCGTCGCGTTGCGG
 CCGGCTTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGGCTCTGTGGTCTGGTTCATCTTGG
 TCCATGTGACCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACCTTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCTCGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTCACTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCCTTATCACAGCTGGAGGGTCCCTCCGAAGTATTACGCGCAGCC
 TCTTGTGTAAGGACT**TGACT**ACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCCAGCCCCAGCCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTTGGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTCAGCCAGTCAGTGACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTCTGCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCCCTCTGACGGCCGACGGCAGGAGGACAGTGGGGTAT
 GGTGTATTCTGCCCCTGCGCATCCCAACCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGG
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGACCTAGTTTAGCCATTGCCTTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCTGAGGGGGGAACCATTTTTGGGTGTGATAAAATACCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTAAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCT
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAAGTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCAACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAAGTGCACCTGGAGGATCAGACTACCATGACATCGTAGGGGAAGGAGG
 GAGATTTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGGGGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTTCTGCTGAGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAATTTGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

0
1
2
3
4
5
6
7
8
9
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U
V
W
X
Y
Z

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTGGGATCCATGGAGAC
 TCACCCATTANTTCTTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCGTGTCCTGGTCAGGCCCCACCCCCCTTCCCACTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTCGGCCCGGCCCTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTGCGGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTGTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGTGCCAGAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAACCTGGTGAGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGCTGTGCGTCTGCACCCACATCTTTCTCTGTGCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTGTGTGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCCGGTGGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGCTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACGAACAGAAGAATTGCTCCCACTAAAGATGTGACAGCCAT
 CAACGTCTCCTCTCATTTGCCCTCTGTGCGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGCTCTGGGGAGATTACCTTGTGCCCCGGCCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCAGCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTGCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAATGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPWMVLCALITALLGVTEHVLANNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQFPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGDSGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

ATGAGTCAACGACGCGGGAAGAACCATGGGCGGGCTGCCCAACTTGAGGAAGGGCGCGCACT
CAAGCGACGCGCGAGCTGCGGCTACGTGCTGTCAGCGTGTCTGCGCCCTGGCTGTGCTG
TGCTGGCTGTAGCTGTCAACGGTGCCTGCTCTTCTGTCAACCAAGCCACGCGCGGAGCG
CGCCGCCCACTGTCTGCAGCACTGGGGCTGCGACGCAACAGCGCCCTGTGCTATGTGA
AAGGTCGGGACGCTGCGACCTCAGCATCTCTATGACCCGCGCTGCCCCAGCTCACCAGCA
GCTTCGCAACGCTGGAGAGCCGCCAGGCGCTGGTGCTGACGGCGTGACAGCAGCAGGCG
CAGCGACGCGCTGTGGGCGACCAAGGACAGGAGCTGCTGGACACCTGCCGCGACAGCTGCC
CCGCTGTCTGGCCGAGCTCAGAGCTGACAGCGAGTGACATGGGGCTGCGGAAGGGGATGT
CGACGCTGGGCGAGGCGCTCAGCGCCTGCAAGTGTGAGACAGGCGCGCTCATCAGCTTCTG
TCTGAGAGCGAGGCGACATGCTCACTGGTGAACCTCGTGACGACATCTCGGATGCTCC
CGACAGGGACCGGGGGCTGGGCGCCCGGCAACAAAGGCGCACTCAGAGAGCGCTGCC
GGGAAGCCGGCCCGGGGCTGTGCCACTGGCTCCCGGGCCGAGACTGTCTGGAGCTCTCT
CTAAGCGGACAGGACGAGGACATGGCTGTACTCTGTTTCTTCCACCACCTACCGCGCGCTT
CCAGGTGTACTGTGACATGCGACGACGCGCGCGCTGGACGGTGTTTACGCGCGGGAGG
ACGGCTCGGTGAACCTTCTCCGGGCTGGACGCGCTACGAGACAGCGGTTTGGCAGAGCTCC
GGGAGCACTGGCTAGGCTCAAGAGGATCAACGCCCTGACCAACAGGCTGCCTACGAGCT
GCACGTGGACCTGGAGACCTTTGAGAATGGCAGGCCATATGCCCGCTACGGGAGCTTCCGG
TGGGCTGTCTCTCGTGACCTTGAGGAAGCAGGTTACCGCTTACCGTGGCTGACTATTCC
GGCATCGCAGGCGACTCCCTCTGAAGCAAGCGGCATGAGTTTACCAACAGGACCGCTGA
CAGCGACCATTCAGAAAGAACTGTGCGCCCTTACCGGGCTGGCTGGTGGTAGCCAACT
GCCACAGCTCCAACCTCAATGGCGAGTACTCTGCGGGTGGCGCAGCGCTCTATGCGCAGCG
GTGAGTGTGCTCTCTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGTAGAAGATCCG
CGCGGTCCGGGAGAGCGCTAGACTGGTGCACTGTGCTCTGGCCGCTGCTGTCTCTGTGCG
CCCATCCCGACCCCACTCACTCTTTCTGTAATGTCTTCCACCCACTGTGCCCTGGGAG
CCACTCTCCAGTAGGAGGGGCGGGGCCATCTCTGACAGAGCTCCCTGGGCGGTGAAGT
CACACATCGCTTCTGCGCTCCCAACCCCTCATTTGGCAGCTCACTGATCTTGTGCTCT
TGCTGATGGGGGCTGGCAAACTTGACGCCAACTCTGCTGCTGCCCCACTGTGATCTCCGG
TGCTGTTTGGCGTCCCTCGCCAGGATGTTGAGATCTGCCACGAGCCCTGCTGCCCTGCC
GGCCAAATACCGGGCATTTATGGGACAGAGAGCGGGGCGACAGACCCCTGGATGCTCT
CTACAGAGTCTGGGGGAATGTGAGGCTCTCTGAGGTAGGTTGAGGCCCTGATCTCCAG
CCCTCCCAATGCCAACCCCAACCGCTTCCCTGGTGCGCAGAGAACCACCTCTCCCAAA
GGGCTCAGCCTGGCTGTGGGCTGGGTGGGCCCATCTACAGGCGCTGAGTGCAGGATGGG
GAGCTGTGCTGCCCTTGGGGACCAAGCTCAAGGCTGAGACAGTTCCTCGAGGCGCACCA
CCTGTGCCCGCGCAGGCTGGGGTGTGAGCTCTTATACCTGCTGTGCCACCTGCTCTGT
TCTCAATTAGGCGCAACCTCCCGCCACCAAGCTCCGGGCTGCTCTCACTGGGCGAGC
CGGGCTGCGCATCCCATTTCTCTGCTCTTGAAGGTTGGGTTGGGCGCTGCACCTGTGGGCT
GGACTCTACCTCTATGGGAAGCTCTGTGTTTCTGGGCTGGGCGCTAGGCGAGGCTGGGATGAG
GCTGTACCTCTGAGCAATATGAGGCTCCAGGAGCTCAGGCTCTGAGGCTCCGAGGAGG
CGCTTGGGTGATGGCCCTGTGAGGCTGTGAGGCTGATGATGATGATGATGATGATGAT
ATTGACCTGGGCACTGCACCGAGCGCGGCGCGCGCGGCTGATGAGGAGCAGGAGCA
CCACTACCGGGCAATGGGCTGGGGGAGCTGGGCGACGACGACCTCACTGAGTGG
CTTTCTGTTGTAATCTCCCAACCCAGCAGCTGTCACTCCCACTCTCTGTGCACACA
TGACAGGTTGAGACCCGAGGCTCCAGGACGAGCAGCCAAAGGCGAGGCTGGAGCCGG
TCTCTAGCTTCTGCTCAGCGCTCAGACCGCTGCGCTTACCTCAGGCGCCAGTGTACGG
CGGCTGTCTCAAGGCGTCTCTGATGGGGGCTCCGAAAGGCTGGAGTCAAGCTTGGGAGCT
GGCTAGCAGCTCTCTCTCGGCGACGAGGGAGGTTGGCTTCTCCAAAGGACACCCGATGCG
GGTCTAGGGGGTGTGGGGTTCTGTTTCTCCCTTCCCTTCCCACTGAAGTTGTGCTTAA
AATCAATAAATGTACTTGGCCACATCTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCT
TGCTCCAGTGTGCCAACAGGCTATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLDTLADQLPRLARASELQTECMGLRKHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLARGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGCGCGCCAGGGCAATCCGACCACATTTCACTCT
 CACGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGCTGCAGCATGTGGC
 TGA AAAA CTCTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTCTTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAACAAACAAGAAGA
 CCTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTGCGC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTCTGTTCAAGATCACCAGCATTCTTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTTACATGCCCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAA CTTT TAGCTCTCTTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTCAT
 GTCTTCTTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTGTGTTGTTTCAGTTTACATACTAGTCCCTTCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCATTCTTCTTCCATTGACCCATATTTATACCTTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL
LYNKAGAHRCSPCTEQWKWHGDNQYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFA
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPPTSELFHIIIDVTSPRSRDCVAILNGMIFSK
CKELKRCVCERRAGMVKPESLHVPPETLGED

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC



FIGURE 232

GCGGAGCGCAAGAACCTTGCAGAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCCGCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTTCGCGCGGGGCGGGGACCCGCGGTTCGGGCGGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCGCCGAGGGCCCGTGGCCGTGGGCGATCTCCCTGGGCTTACCCGTAGCGCT
 GCTAGCTTCACTTGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCACTGTGAGACTCTG
 AGCTGCCGCCGCGCGCAACCAACGCGCGCGCGCGGCCCACTCGGTGACAGCCCGAGCG
 GAGCGCGAGAAGCCCGGGGCCGCGAAGCGCGCGGGGAGAATTGGGAGCCGCGCTCTTGCC
 CTACCACCTGACAGCCCGGCCAGGCCGCCAAAAAGGCCGTACGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCAGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCCCGCGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCCTTCTGGTGCCTGACACCACTACACCGAGGCGCACGGCCTGGCAGCGCTTAACCTGG
 CCACCTCAGCCTGGCCCTCGCGGCCCACTGTACTTGGGCGGGCCAGGACTTATCAGCGG
 GAGAGCCCAACCCCGCCCTACTGCCACGGAGGCTTTGGGGTGTGCTGCTGCGCGCATGCTG
 CTGCAACAACCTGCGCCCCACTTGGAAAGGCTGCCCAACGACATCTGCTAGTCGGCGCCCTGA
 CAGTGGCTGGGTGCTGCTGCATTCTCGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG
 GGGTGACATATAGCCATCTGGAGCTGAGCCCTGGGGAGGCCAGTGCAGGAGGGGGACCCCTCAT
 TTCCGAATGCGCTGACAGCCCACTGTGCGTGACCTGTGCGATGTACAGATGTACAGCTGCACAA
 AGCTTTCGCCCCAGAGCTGAACCTGGAACGCACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCAAGCCATCTGGCCGTTGATGGGGACCGGCGAGCTGTGGCCCTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTGGAGGTGCTGCGCTGGGACTACTTACGGAGCA
 GCACGCTTTCTCCTGCGCCGATGGCTCACCCCGCTGCCACTGCTGGGGCTGACCCGGCTG
 ATGTGGCCGATGTCTTGGGACAGCTCTAGAGGAGCTGAACCGCGCTTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGTTTGTATCCGGCCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCGCGGCCCTCACTC
 GCCGAGTGCGAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGCTCACT
 GAGGCGCTCAGCTCTCACTGTGCTGTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG
 TCTTCTGGAGGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCACGCGGTGGCCATGCAGATGTCTTCGCACTT
 GTCAAGGCCACAGTGGCAGAGCTGGAGCGGCTTTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCGCACCTTCACTGCGCTCATGGATCTACTCTCCAAGAAGACCCCGC
 TGGACACATGTTCTGCTGGCCGGGCCAGACAGCGTGCTCAGCGCTGACTTCTGAACCGC
 TGGCCATGCATGCCATCTCCGCTGGCAGGCTTTTTCATGCAATTTCCAAGCTTTCCA
 CCCAGGTGTGGCCCCACCACAAGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCGCCAGCGAGGCGCTTCTCAACAACCTCGACTACGTGGCAGCCCGTG
 CGCCTGCGCGGACGCTCAGAACAAAGAGGAGCTGCTGGAGAGCTGGATGTGTACAGCT
 GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCCGCCAGAGCTGCGAGCGCAGGCTCAGTGAGGACCTTACACCGCTGCTCCAGAGC
 TGCTTGGAGGCGCTCGGCTCCCAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCAGCT**AG**ACCCACCTGTCCCGTGGCGGTGGCATGGCCACACCCACCCCACTT
 CTCCCCAAAACAGAGCCACTGCCAGCTGCTGGGCGAGGCTGGCGCTAGCCAGACCCC
 AAGCTGGCCCACTGGTCCCTCTCTGGCTCTGTGGTCCCTGGGCTCTGGAACAGCAGTGGG
 GGACGTGCCCCAGAGGACCCCACTTCTCATCCAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTCCGGCTGTGGCCCTCACGATTTATGCACTACAGCTGTGCCGTGAGCCGACCCCTG
 CTCTGGGCGCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCAACATCTCCCTTTTGACCTGCCGAAGCTCCCTGCCTTAATAAATCGGCCA
 AGTGTGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDEFDWFLLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAFVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTFLLAGPDTVL
TPDFLNRCRMHAISGWQAFPMHFQAFHFGVAPPQGGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCIQSVLEGLGSRITQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAATCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCT
 TTCCCCGCCCCTGAGACCCTGCAGACCATCTGT**CATG**CGGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGCAGCGGCACGCGAGGGCTCCCGGCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGCTCTTT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACCCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGTTCGACCCAGCA
AGATCCAG

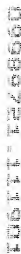


FIGURE 237

GCGGCGGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGTCTCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAAACCCACGGGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTCCGGAGCTTCAGCGGGAGGAGTG
 TCCCATTTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGGAGGACCCGATACCTGGGGGCCACCCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAAGTACCCTCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAAGTTGATTGTGATGCCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCCTCTTCCGGATGTTCTCCCGAACCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCTCCTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAAGAGACCCCAAGAGAATGAGGCCCCCCAGTGCCCTTCTGTC
 ATGCCACGCGGTACGTGAGTGGCTATGGGCTGCAGAAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCCTTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGTGCAACCCACCTCCTGGAGATGCTGATTAGCTGCCG
 GCCAATCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCCATCTGTCTCAGCGCCCTTGTCGCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTGTATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGGCCAAGCGGGTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**TA**ATT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCTGGACCAGGTCAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTTGAATTA
 CTTAGAAATTCATTTCTCACTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGTCCGTGGCTGCTGTATTGGACAGCAGAAAAAGATTTCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAAAAGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEFPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
 RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
 ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
 KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSIWELRQTLVVVFDAFITG
 QGKKDWSLFRMFSTRLTTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
 YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
 PYRAFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
 VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
 GSNYFVRLYTEPLLNLPTPDFSMPYNVICLTCTVAVCYGSFYNNLLTRTFHIEEPRTGGLA
 KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATTGATGTCTGGGTCTTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLTVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 241

[illegible]

FIGURE 242

MRSCLWRCRHLSSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSOAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDGRKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSRPGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKPQATPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPFGFMELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWELEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
 RYMKNRFLRSKTLDGAAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYIDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CG**ATG**CGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAG**TGA**GCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCCACCCCGGCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCGGGCGCGCGCG
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTA**ACT**GCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTGGGGTGGCAGGAGTCCTCCAGCCACCAAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACCTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPITAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPPP
YMPQPSPYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCCAAGGGTAGGGCGCGCCCAAGAT
CCCCAGGTAGGTAGGACGAAGAAGATGGCGTGTTCCTGCCCTCAAAATGGTCCCTCGCAACCTAT
TCATTTCATTCTTCCCTCACTGTATGGCTCTCTTAAGTGTGTCACCTCTTCATGGTGTACAGAT
CTGACGAAGCATCTCCAAAGCTGTAGTGATGGGACCACTTCCCTTGGAAATAAAATACGACTTCT
CTAGTAGCTCATCCCAAGTCTATTATGATCTCTGTATCCATCGAAACCTTCCACCGCTGACC
TCTTGGGGAAACCAGAAATAGAAATACACGCCAGTCAAGCCACCCAGCAGCATCATCTGCA
TAGTCAACCACTCGAGATATCTAGGGCCACCTCAGGAAGGGGAGCTGGAGAGGGCTATCTCG
AAGAACAACCTCGAGGTTCTGGAAACCCCTCTCAGGACCAAAATGTCATGCTGGCTCCCGAG
CCCCCTCTTGTGGGCTCCCGCTACACAGTTGTCAATTCTACTATGCTGGCAACTTCTGGAGA
TTTCCACGGATTTTACAAAGAACCTTACGAACCAAGGAAGGGGAACCTGAGGATATCTAGCA
CAACACAAATTTGAACCACCTCGAGCTAGAAATGGCTTTCCTCTTGATGAACCTGCCCTT
AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCTCAAGGACCACTAGGCATCTCAACATCT
ATTGTTGAATCTGTGACTGTGTCTGAGAGGACTCATAGAAGACCTTTTGATGTCACTGTGA
AGATGAGCACTTATCTGGTGGCTCTCATCATTTTCAGATTTTGAGTCTGTGACGACAGATAAAC
AAGAGTGGAGTCAAGGTTTCTGTGTATGCTGTGCAGACAGAAGATAAATAGCAGCAATGCT
ACTGGATGCTCGGGTGACTCTCTAGAAATTTTATGAGGATTTTATCAATATATGTTATCT
CTGACCAAAACAAGATCTTGTCTGCTATTTCCGATTTTTCAGTTGTGTCATAGAAATCTGGGA
CTGACAAACATATAGAAATCTGCTCTGTGTGTTGTCGAGAAAGGCTTCCTGCTCAAGTAA
GCTTGGCATACAGTACGCTGTGGCCCATGAAGTCGACACTGCTGTTTGGGAACCTGGTCA
CATGGAATGGTGGAAATGATCTTTGGCTCAAAATGAGGATTTTAAATTTATGAGGTTTGT
TCTGTCAGTGTGGACCATATGGAACCTAAAGTGGAGATTTATCTTCTTGGCAAAATGTTTGA
CGCAATGGAGTAGAGCTCTTAAATCTGCTGCTGCTGCTCACTCTGGAAATCTGTG
CTCAGACCGGGAGATGCTTAAATCTTCTATGATGAAGGAGCTTGTATCTGAATATCT
CTAAGGGAGACATCAACCGCAGCGCATTTTAAAGTGTGTTATTCACAGTATCTCCAGAAGCA
TAGCTTAAATATACAAAAAGCAAGGACCTCTGGGATAGTATGCGACGATTTTGGCTACAG
ATGGTGTGAAGGATGAGTGTGCTTTTGTCTAGAAATCAACATCTCATCTTCATCTCATAT
TCTCATGAAGGAGGGTGATGTGAACACATGTAACACCTTGGACATGACAGGGGTTT
AGGCTATCGAGCGCGCCCGGACCTTGGGTACCTGTGGCATGTTCATTTGACATTCATACC
AGCAATCAACAACTGTCTCATGATTTTGTCAAAAACAAAACAGATGTGCTCATCTCC
AGAAGAGGTGGAATGCAATCAAAATTAATGTGGCCATGAATGGCTATTACATGTGCTATTAG
AGGATGATGCTAGGGAATTTTACGTGGCTTTTAAAGGAACACACACAGCAGTCAAGCAT
AATGATCGGGCAAGTCTCATTAACAAATGCATTTCACTCGTCAAGCTTGGGAAGCTGTGCAT
TGAAGAAGCTTGATTTTATCTCTGTACTTGAACAAATGAACATGAATTTCTGCCGTGTTC
AAGGTTTGAATGAGCTGATCTCATATGTATAGTATTAAGAGAAAGAGATATGAATGAAGT
GAAGCTCAATTCAGGCCCTCTCATAGGCTGTTAAGGCACTTATGATAGACAGCATG
GACAGCAGGGGCTCAGTCTCAGAGCAAACTCTCGGGATGAACACTACTCTCCGCTGTG
TGCACAACTCATCAGCCGTGCTGTACAGAGGGCAGAGGCTATTTCAGAAAGTGAAGAGAACTC
AATGGAACCTTGAGGCTGCCGTGTCAGCTGACCTTGGCAGTGTGCTGTGGGGGGCCAGAG
CACAGAAGGCTGGGATTTCTTTATAGTAATAATCAGTTTCTTTCTGTACAGTATCGAGAA
GCCAAATGAATTTGCCCTCTGCAAGACCCAAATTAAGAAAGACTTCAATGGCTACTAGAT
GAAACGTTTAAAGGAGATAAAATAAAAACTCAGAGTTTCCCAAAATTTTACACTCATTTG
CAGGAACCCAGTAGGATACCACTCGGCTGGCAATTTCTGAGAGAAAACGGAACCAAACTT
TACAAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTATGGGTACAAACAAATCAA
TTCTCCAGAACCAAGCCGCTGAAGAGAGTAAAGGATTTCTCAGCTCTTGAAGAGAAATGG
TTCTCAGTCCGTTGTGTCCAACAGCAATTAACCAATTTGAGAGAAACATCGTTGGATGG
ATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAGGTGAAAGCTTGAACGTATCTAA
TTCTTCCCTTGGCGGTTTCTGTGTATCTCTAATCAACCAACTTTTGTGTAGTGTATTTCAA
ACTAGAGATGGCTGTTTGGTCCCAACTGGAGATCACTTTTCTCCCTCAACCTATTTTTGA
CTATCCCTGTGAAAGAAATAGCTGTAGTTTCTTATGAATGGGCTTTTCTATGAATGGGCTA
TCGCTACCATGTGTTTGTCTCAACAGGTGTGGCCTGCAACGTAAACCCAAAGTGTGGGT
TCCCTGCCCAGAGAATAAATACCTTTATTTCTTCAAAAAAATAAAAAAATAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVK MSTYLVA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVLTLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAEHLAHQWFGNLTMEWNNDL
 WLNIEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFTITSKNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLV SIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKMRDMNEVETQFKAFILRLRLDLIDKQTTWTDGSGVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPVDVTIAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKELQWLLDESFKGDKIKTQEFQILTLIGRNPVGYPYPLAWQFLRKNWNKLVQKFELGS
 SSI AHMVMGTTNQFSTRTRLEE VKGFFSSLKENGSQLRCVQQT IETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTACAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCAGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTATCGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGGCTAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAATCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCCGGCAGTGTC
 CTACCTGTGTGCAGCCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTACGGGCTGCGTGGGCCAACCTTCCAGCTTCTTGTGAACCAACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCCTCCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTT
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWVSDLPQWTFKNTSCDSGLGCQDTLMLI
ESGFPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC
PSC



FIGURE 251

GCGACGGGCGAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATCGGGGAGAGAAGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGACGCTGAGCATGCCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCCAACAAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**CGCTCAGGCTGGGGCTGCCCATTTGGGGGCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAG
 GCTCACTGAGTAGAGGGCTGTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCCTGGGGTGCTGTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTATCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

252/330

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCCCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCAGCTCCTGTTACCCCTTCTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGGAAGTGC
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCCTGTAGTGT
CCTACATTAATAATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTPEKRDMDHDFVGLMGKRSVQPEGKTGFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCTCTGTGCG
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCCTGGGTGGTGCATCCCCCTTGGGGC
 TGCTGTTCTGCTGCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAAATACCAGCACACGAGTCTCACTCCCGGTCGCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCGGCTCCGGCCGAGAGGCTGGCACCAGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCCACCTGGAGGCAGAGTGGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACC GGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCCTTCTCGGCTGGTTTTCCAGAATAACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGACCACTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

256/330

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGGCCACCGGGACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCTCTTGAACCTCCTTGGCAGCTCACATGGAACAGGGCCG
GTATGACTTTCGAACCTGAAGTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACCACTGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCTCTTCTGGCCGGGCTTTTGGCCGGGGCTCAGGAGGAGCAGGCCACCTTGTCTTT
CAGCAGGCCGCCACCTTCTGATGGTGCATAAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCTCC
CTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTGGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGGCCCTTGAGACATCCTT
 GAGAAAGGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTCTCGCCCGCCGCGAGTGATC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAAGTGATCCCAAGCAACGAGGGGCATACATTCAAGAATTCGAAGAGTTCTCAAAAATATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAAGTGCAGTGGGTAACTT
 GGCACCTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAAATACCTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAGAATGCTGTCTATA
 ACTCTCCAAAGGTGACTTATTAATTTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTATGGAGGATAACACCAAGCCAGCTCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGGCTCTGGGCCATCCACTCTGGGCCAGGCCACCCATAGCCATTTGGTCTCTCA
 AAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTATGGGATACCCCATCGAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGCCCA
 GGGCCCTCATCGCATCACTGTCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTGTTTCTTCCCAAGAGACCAAGAAGTCACCTCATGATCCATTACAAACCCAGAGAT
 AAGCAGCTCTATGCCCTGGAATGAAGGAAACAGATCATTACAAACTCCAGACAAGAGAGAAA
 GCTGCCCTCTGAAGTAATGCATTACAGCTGTGAGAAAGAGCACTGGCTTTGGCAGCTGTTCT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTCCTTCCCAAATGTCAGTGCCTTAGGTATCTTCTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCAAAC
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCCTTTGTGTTTACT
 GCTCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCGACAATTAGAGTTGTATGCCAGC
 CCCTAATATTACCACTGGCTTTTCTCTCCCCTGGCCTTGTCTGAAGCTCTTCCCTCTTTTTT
 CAAATGTCTATTGATATTCTCCCAATTTTCACTGCCCAACTAAAATACATTAAATATTTCTTTT
 CTTTTCTTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCTCCATGCCCTGTCT
 CTTCCTACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTCATCATTTGAATTTCTCGTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCAATTCAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAACTACTACAAATCCCTAGTTTTTTCCATTGCCCAAGGAAGCATCAATACGTATGTT
 TGTTCACTACTCTTATAGTCAATGCGTTTCTCGTTTCAAGCTTAAATATATAGTCTGTGCC
 TTTAGCCAGTTTTATGTCTGCACAAGACCTTTCAATAGGCCCTTTCAATGATAATCTCTCC
 AGAAAACCAAGTCTAAGGTGAGGACCCCACTCTAGCCTCCTCTGTGCTTGTCTGCTCTGTCTGT
 TTCTCTCTCTCTGCTGTTTAAATCAATAAAAGTGACACTGAGCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLEMLL
QEAEEEKKIRTLNLASCDNMLGKLSLKIVKMMDTHGSWMKDVAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWSQGTQGVYKGLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTSYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSDWT
PCRSQDAEASFLLCGVLVYVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPSSHSMIH
YNPRDKQLYAWNEGNQIIYKLTQKRKLPLK

FIGURE 264

MELSQMSELMGLSVLLGLLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRKEKPPQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDITVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTRFEAAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGTCTC
 TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGGTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCCTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCA
 CCAATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCGTATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCCTCCCTCCCGAGGTGACCTGCTCTCTTCTTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCAGGTCCCTGGCTGACCCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCAATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

266/330

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAGGGAGGCACCTTGAGAAATGTCTTTTC
 CTCAGGACCCAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCAAGACTTTGGCCTCAGAGAAAAATTGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACCTTGGGAGGCCAAGG
 TGAGCAAGTCACCTTGAGGTGCGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKITLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGACAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGTCCCCCTCTCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACATATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGCAGGGGTGTAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

0908724-11001

[illegible]

FIGURE 274

MGLFRGFVFLVLVCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQFFYRAKSKKIEATR
 CSAGISGRNRVYKQCGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMSIDSVSVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQIRIVCLV
 LDKSGSMGGKDRNLNRMQAAKHFLQLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGRYSCLKVRAHG
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFDVGKVRYYIIRISASILDRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFIILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CTCTTAGGTGGAACACGGGGATAGAGTACTGACAGCAAAAGCCGGGAAAGACATACGTCGCCG
GGCAGGGGTGACAAACAGGTGCTATCTTTTGATCTGCTGCTGGCTCTGCTTCTATCAAGGAAG
ACCGCAAGGTAAATTTTGACCACAGGACGAATGATCTAGCACACCGCTCTTCTGCTGATGAC
CCAGGATTGCGCAGGATTTACTAGAGAGTGTCAACTCAACACGAGCGGCTCTTCTGCGTATCTCT
GTGTTTGAGGAGAGACAACTTTGTGGGCTGCTTCTTATGAGTGTCTCAAGAGTACTTGCCTGA
GGGTGGACCGAGAAAGAAAGAAAGTCCCTCTTCTGCTTGCTGCACATCAGGAAGGCTGTGATGG
AATGAAGGTGAAATCTTGGAGATTTCACTTCAGTCACTTGCCTTGCCTGCAAGATCTCTTTAAAA
GTAGAGAAGCTCTGCTGTGTGTGTGTTAACTCAAGAGCGCAACTCTGCTTAGAAGGAATGGATG
CAACGAGCTCCGGGGCCCCAACCGCATGCTTCTGTGTGTAGCCGAGGAGAGCCCTTTCGTGGGG
GCCCGCGCTTTGGAGGATGCCACCGGTTGTGGACGAGTGGCTGATTTCTGAATGATGATGTTTCGG
GGGGGCTGTTCTGCTGGATTTCTCCGGGTGTGGTTTTCTGTGGTGTCTCTGCTGTGCTATCTGT
CTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGAGCTGGCAGTCCCGAGGCCCAACAGC
CCCACGGGGAAGGAGGGGTACAGGCGCTCTCTCAGGATGGGAGGAGCAGCCGCACTACGCTGA
CGCCTCTGAACGCGCATACGACAGTCAAGGAGAGCTCGAGGAGGAGTGAAGCATCTCAGAA
CGCTCTGACCAAGCAGCATGCTCTGGCTGGCTCTGCAGAGGAGGCCCCACAGAGAAACCCAG
CGCAGCTCTCTCTGCTGCTGGGTGACAGCGAGGAGGAGGAGTGAATCTGGCGCTCAGCTGG
CCACAGATGCTCGACGATGCTTCTCTGCTGCTGACAGCGAGGAGTGAATCTCAGCTCGACATG
CCTTACGCCGCCACCCAGGAGAACGCTTGTGAGAGAGGACAACTGAGGAGTGAATCTGCTGCT
GAATCAGCTTTGGAGAGCTGAACAATCTCGCAGAGAACAGCCCAATCAGCTGCTCTTACCGCT
CTGATTTTATAGAAGGATCTTACGAAACAGGAAGGACAAAGGACCATGTATGAGCTCAGCTCAA
AGGGGACCAAAACGCAATTAACCGCTCATCTATTTCGACCATCAGCGCCATCATGAAGT
AAAAATGAAAGCTCAACATGGCCAAACCGCTTATCATGTATTCTGTCGCTACGAAAAGGGTGG
ACAAGTTCCGGCAGTTCATGCAAAATTCCGGGAGATGTGCATTCAGCAGGATGGGAGATCCAT
CAGCTGTGTTTCTTTGGGAAGAAGAAATAAATGAAGTCAGAAAGGAATCTTGGAAACACTTCAA
GCTGGCCAACTTCAGGAATCTTAACTTCATCCAGCTGAATGGAAGATTTCTCGGGAAGGAGCT
ATGTTGAGCGCGCTCTTGGAAAGGGAAGCAACGCTCTTCTCTTTTCTGTGATGTGCATCACT
TCTCTGAATCTCTCAATACGCTAGGCTGAATACACAGCCAGCATGATCGAGTCCCTCCTTGGAAAC
TCTCTTCAGAGAGTCTGAGTCTGATATACGCGCATGATGATGGATGGATCTGAGCTGAGATCG
AGCTGGTCTATAAGAGAGAAAGCGGTTTTCTGCTGATGATGATGATGATGATGATGATGATG
TCCAGACTTCATCAATATAGTGGTTTTGATCTGATGATGATGATGATGATGATGATGATGATG
CTTTTATCGAAGTATCTCCACAGCAACCTCATATGTCTTACCGACGCTCTGCGGAGACTTCTCAC
TCTGGCATGAGAAGCGCTGCATGACGAGTGCACCCGAGCAGTCAAGAATGTGCATGCTGACCA
GGCCATGAACCGGAGCTCATCCGCGGCACTGGGATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
TCTCGCAAAAGAAACAGAGACAGCAAGTAGCAAAAAAACCTGAATCCCAAGAGAAGATTGTGGGA
CACTTTTTTCTTTCTTTGCAATTACTGAAGTGGGCTGCAACAGAGAAAGACTTCCATAAAGGAC
ACAAAAGATTTGGAATGATGGTGAGATGAGAAGAGAAAGCTCGGATTTCTCTCTGTGGGCTTTTAC
AACAGAAATCAAAATCTCCGCTTTGCTCGTAAAGGATTAACCCAGTTGTCACGCTGGAAGTGTCTGAC
AAGGCAAGATGCTGTGAGATTAAGCTTAATGGTGTGGAGGTTTTGATGGTGTTTACAATACACT
GAGACTGTGTTGTTGTGCTCATGAAATATGATGATGATTAAAGACAGTTTGTGAATAAATTCAT
TCTGATG
AATGCTAAAAATCAGAAGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG
ATAATAATGACACAGAAAGAAAGAACCATATATATATATATATATATATATATATATATAT
AAAAATATGCTTATCTTTTGGTGTGCTTTTAACTGTCTCGTTTTTCTTTTATATATATAT
GCATCTTTTTTCCCTGTGAGTTATAGTCTGCTTATTTAATACCATTTCGAAGCTTACAGAGA
GCAAGTGTGGCTACATTTTATATTTTAAAGAATACTTTGAGATGCATTTAGAAACTTTCA
GTTCAAGACATCAAAATGTGACCATTCAGGAGCATGCCAAATGCTGATTCTGAGGCACCTGAAT
GTAGGACTTGAAGCATAGGGAAGGAATGGTTGTACTAATACAGACGACAGATGATCTTCTGGA
GATGATTTTGAAGGAGGACAATGAACACTGGAGGAAAGAAATGACACTTCTGCTTTACAGAA
AAGGAACACTCATCAGACTGGTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGAT
GAGTAGGGAGCGGCTTTCTTACCTGTTTAAATAAACCAAGATGACCGTGTGAACCAACCAATCTCT
TTTAAATAACAGGTTGCTCTCTCGGCTTCTGGCTTCATAGAAGAAGAAATGGAGAAAATATATAT
GTTATTCACATCTCTGAGGAAGCATCATCTGCGCAAGATCTAGTGGGATGGAGTTTGTGCTACAT
GTTATTCACATCTCTGAGGAAGCATCATCTGCGCAAGATCTTAAATTAAGCAGTTTCTACATCA
CCAGATGCTCTGAAATTCGATTTTATATATTTTATATATTTTAAATTAAGCAGTTTCTACATCA
ACATAGAGTGTTTTCTTCTATCTGATGAAATTTATAGCAGCCAGCATCTGATGATGATGATGAT
CTTTGAGTCTGCTGCTTCTGTTGCTGCACAGTAACATCTGTTTAAAGCTTCAGAAGATCTCAAG
TGTTGTGTTGTAAAAAATGATTTGATTTGATGATGATGATGATGATGATGATGATGATGATGAT
AGGCCATGAATGGAGGTGATATTGCACAGCTAATAAATATGATTTGTGATATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSKKT

FIGURE 277

GAAAGA**ATG**TTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAC
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCA**TGA**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATCTCTCTTTGTAATAAATTTGAATGTGCT
 TGAAAGTGAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAAAATTTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCCTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCAATAGGAC
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP



FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATG**T
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACCTTCTCCAGCTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTCCAAGAACA
 GAACCTAGTATTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGCTGTACATTCTCTTCCAGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCTTCCACATCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAAGATAAATCTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACATAGACACATCTTGTCTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLEDTD

280/330

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCCATGAAGTTCTTAGCAGTCCTGGT
ACTCTGGGAGTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTTCATGCTTCCTGTGATTTC
ATCCAACCTACTTACCTTGCCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA



282/330

FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

0
0
0
0
0
4
U
U
A
A
A
A
0
0
A

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATAAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNRVWAPATESSAQLCCWPVGVARGGALCQ

17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCTTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCCT**TGA**ATCTGCCTGGATGGAATGAG
GACCAATCATGCTGCAAGGAACACTTCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTACTGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

Figure 1 displays a series of 12 line drawings illustrating the progression of a child's drawing of a person from age 2 to age 11. The drawings are arranged vertically, with the youngest at the top and the oldest at the bottom. Each drawing is labeled with an age: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13. The drawings show a clear development from simple, abstract shapes to more detailed, human-like figures.

MPVPALCLLWALAMVTRPASAAPMGGPQLAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRITIELLGGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCAGAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAATCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTGCTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAAATAGGCTCTTTCTCCAATGTGTCTCCAAGCAAGATTTCATATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACCTTTTCAGCCTGTTGCTCATCTGTCCATGTGGCAATAATACC
 TTGTCAGCCCATACCCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGTAT
 CAATTTTTCATTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGAAAATTGCATACGCTGTGCAATT
 TTTTATCTGCTAGTGCTATTCTGCTTGTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATTACAAGTTTAGACTTGAGGGGAAATGGGCTTTTTAGAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTGTAGCTGTTTTCATTTGCTCA
 ATAATAAGCCTGAATTCGTATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTCCCCGCGCGC
CCCGAGCCCCGCGCC**CATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGCGGGACCCTGCCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGC**TGAG**CCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
217

FIGURE 291

TGAAGGACTTTTCCAGGACCCAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGACGCCGATCACATGAAGGTGGTGCCAAAGTCTCTGCTCTCCGTCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCCAGACAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGACAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCCAACG
 CCCGGCTCTCTGCCTTCCCTCTTAAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAGAGACTCGGGGAAAAATTCCCAAAC
 GTTTGATGAGATTAACTCTGAAACCAAATTAATTTCTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCCTGTCTTCAACGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGACGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCCAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCCAGAAACATGGAAGTTTTCTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGCAAAATTAC
 TGCTTATTTCCATGCCTCTGTGCATCAAAGTGGACCGGCCATTTCCATTTGATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCTGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCTATGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGAAGGGGAGAATTCA
 CATCTGGGTGGACAGAGCAGGACGATGCAAGATTCCATCCCCTACTCAGAATGGCATGCG
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAATTTGATACATATTTTTTAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V I M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVFIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPCLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCTCTGC
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGG**A**CCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACTGCGGGATT
 TGTTCA GTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEGKCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCI GGGGYFPEAS PQQCQDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

296/330

CGCGAGCCGCGCGCGCTGCGCAGAGGAGCCGCTCTCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCTGCCCCGGAACAATGGGACTCGCGCGCGAGGTGCTTGGGCGG
CGTGCTCTCTGGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCGGCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCAACATGTGCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACAGGGATGGTCTCAACAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAAGAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTACAGTAAACATCAACAACACTGCAT
TCTGAAGCAAGAAGAGGATCAAAATTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTC
GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTGGTTTATTAAAGTTTAAAAACAATATTCT
CTTTTGAATAAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAGTCCTATCTTTTTTTTTTGCT
GGGGTGGGGGCATTGGTCCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTGCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACATCAAACTAGACTCTGAAGCATAAATTAAGAAAAACATCAACATTTTTTG
TGCTTTAACTGTAGTAGTGGTCTAGAAACAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVITMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTMTVTNHSSVTSAASSVTITTTMHSEAKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCCG**CATG**CGCACCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGTCTAGCCTGTCTGTCGCTGGCGCTTTCCTGTCTGCTGCTGGC
 GCAGCTGTCTAGACGCCGCCAAGAATTTTCGAGGATGTCTAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCCTCAGC**TAA**TTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAAACCTGGAAGCAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAAAGCACACAGCTCAAAGTCAGCCAATAAGCTTTTCTTATTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT
 CTAATAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTTGTTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATACACATTTG
 TCAGCATTTCCGGTCTGTGGTGAGAGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCCTATGTCTCTTTTGAATGTAACAATAAAAAATAATTTTGAACATCAA

300/330

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII IYLSILGLLLLYMVYLT
LVEPILKRRLF GHAQLIQSDDDIGDHQPFANAHDV LARSRSRANVLNKVEYAAQQRWKLQVQEQ
RKSVFDRHVVL S

300/330

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCAAGGCCCTTCTGTCCC GCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAAATGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTA AAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCA GTTTACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLKAFLSRGKRQEPPTPEGKLGREFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILI
ILHQ

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCTGCTGCCAGTGTAC
 TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTACAGTCTGTATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC CGGTACACTTGATGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCGCCAATGACGGTCCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTTGGGAATTGTC
 TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAG
 AAAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTTGGGCCACTCTACCAGTGATTTTCACTCCCCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAAACCCCCGTT
 GGATCAGACCCTCTGTGGGCAGGGTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAATCAA

MFCPLKLILLPVLLDISYGLNLDNVSPPELTVHVGDSSALMGCVFQSTEDKCFKIDWTLSPG
EHAKDEYVLYYYNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGYTICEIRLKGES
QVFVKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWG HFQNRVNLVGDIFRNDGSI MLQGVRES DGGNYTCSIHLGNLVFKKTI V
LHVSPEEPRTLVTFAALRFLVGGNQLV IIVGIVCATILLPLVILIVKKT CGNKSSVNST
LVKNTKTNKSGEIKEPHFCEGEKHIYSPIIVREVIEEEEFSEKSEATYMTMHPVWPSLR
SDRNNLSLEKKSPIIGGKMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGC AAAGTCATTGAAC TCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTA AAAC TCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAAC TCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAAC TTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

MQDEGDYITLNIKTRKPAIVSVPASSSWRRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFQYVVKQSELKGTKFKGHKSCPCDNTWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGG
CCCGGGGCTGTGGCGTCTGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
GCCCCGGGCAAACGCGAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**CGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGAATGAACAGTGAAGGATACTTGTACACCTCGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTCCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCAGGATCTCAGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAGTTCAAATTTGTGAGTGACATTTACCAAACAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVSFVRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGlnKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGA AAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGAAAAGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAAC TGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGCTGTCGG
 CGCAGCGGCGCCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAC TGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTTCAACCACTTCAACCTGATCCCT
 TGAGGGACTGCTCTACAGTTCGCCGCAATTTACAGCTGAGTGTGCCTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTGTCTTCTGCGCGGGCC
 TGGTACCTCGGCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCTCGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQQLILLISKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAACACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGAATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGALDGT KDDSTNSTLFLNIPVGLRVVAIQGVKTGLY
IAMNGEGYLPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HGBF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAAGTATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AATAAACCCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCCCCCCAAAAAAGGATGATTGGAARTGAAGAACCAGGAGATTCAAAAGAAAAAGTATGTTCAITTT
 TTCTCTATAAAGGAGAAAGTGAAGCAGGAGATATTTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTCTTCTTTCTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGTC
 AAAGAAATTTAGAGAAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATTGACGGATAAATTGCAGTTGGATTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATCTCTTTTGGTATCAAGATCATGCGITTTCTCTTGTTCTTAACACCTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAAGTGTGTAATTCAGAAGGACCAACACCAGATAAATTTATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTTGGTGTCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAAGCAACAGTTTCAGCAAGGTGATTGTGTTTCGGAACCACTGCGTGAGGTTCCGGATGCGATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTCAAGCAGTTCAAGCACTTGA
 GCATTGGAAATCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACATCCATCCGAATGGAGCTTTTGTATACCTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAAACAACCCCATGAAAGCATCCCTCTTATGCTTTTAAACAGAATTCCTCTTT
 GCGCCGACTAGACTTAGGGGAATTGAAAGACTTTATACATCTCAGAAGGTGCTTTGAAGGTCTGTCCAACCT
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAAAGTATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTCGGCTCTTCCAGGGTTTGTATGACCTTCAAAAAGT
 GTGGATGATACAGTCCGATTCAGTGATTGAACGGAATGCCTTTGACAACTTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACAT
 TTACATCAACCCCTTGGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGATGATAAAAGACATGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGAACACTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACACAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTCGAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCTCAAAATGGAACAGCTATGACACA
 TGGGGCGTCAAAAGTGGGAGTGTGCTGCTCAGTGATGGTACGTTAAATTTCAACAATGTAACCTGTGCAAGATA
 CAGGCTGTACACATGTATGGTGAATAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCTGACTGGGAGACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAGGTGCGACGAGAAAACCTTCAACATCCAGTGACTGATATAACACAGTGGGATCCGAGGAAT
 GATGAGGTGATGAAGACTACCAAAATCATATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGTGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGAAAAGCCACCTGCCCTGCTGTGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAGTTAAACAAATAAATCAATACA
 CAGTTTCAGTGCATGAACGTTTATTGATCCGAATGAACCTTAAGACAATGTACAGAGACTCAAAATCTAAACA
 TTTACAGAGTTTCAAAAAACCAACAAATCAAAAAAAGACAGTTTATTAATAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATTATTAATAATCTTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSCVSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGMYTCMVNSVGN
TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTSLTFQ
STRSTKFTTIPVTDINSIGPIDVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDEITGDTFMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GC GCGCGGGAGGCCATCTGCCCCACAGGGGCACGGGGCGCGGGGCGCGCTCCCGCCCGGCACAT
GGCTTGACCGACCTCTGGCGGCACCCAGGCGCGCGCGCCAGCTTGCGCCGAGGTTCGCTCGGA
GGCGCCGGCGCGCCCGGAGCAACGACGAACCTGAGCGGGGAAGCGCCGCGCTCGGGGATC
GGC**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTCACTATTGTTGGAACCTTGGGGATCTCA
CACTTGAGATCAAGAGATGGGAGAGGAAAGGTTCCTGCCCTGCCACCTCAACTGGGG
TTCGACAAAAGAGACCTGTGCATTTGAATGGCTGCTACCGGATAATGAAGGAAACAAAAA
GTGGTGATCACTTACTCCAGTCGTATGTTACATAACTTGACTGAGGACAGGAAGCGCG
AGTGGCCTTTGTTCCAATTTCTGGCAGGAGATGCCCTCTTGAGATTGAACCTTGTAAG
CCAGTGTAGAGGGCGGTACACCTGTAAAGTTAAGAATTAGGGCGCTACGTGTGGAGCCA
GTCACTTTAAAGCTTGTAGTGACCATCAAGCCCAAGTGTGAGTTTGAAGAGAGAGCTGAC
AAGAAGGAAGTGAAGTCACTTGAGTGTGATCATCTCTGGCAGAGAGCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGATGAAGCTTGCTGCCCTCCAAATCTAGGATT
GACTACAACCCAGCTGGACGAGTTTGCTGGCAGAACTTACCATTGCTCTACTCTGGACTGT
CCAGTGACAGCAGGCAACGAAGCTGGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
ATGTACAAAGCATTCGGCATGGTTGCGAGGACAGTGCAGACGATAGTGCTGGAGCCCTGCTG
ATTTTCTCTTGTTGGTGGCTGTAATCCGAAGGAAGCAAGAAAGATATGAGAAGAGA
GAGACCAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTACGCTTGCTGTTCTTCTCCACCTCGCTCCAGCAAAAT
AGTGCTCAAGCAGCGCCAGCGACATGTCTCACTACGACGAGCCCAAGCGAGGCTGGCCAC
CCAGGCATACAGCCTATGTGGGCGCAGAGTGAGAGTTCTGAACCAAGAAAGTCCACCATG
CTAATCTGCACCAAGCAGAAACCAACCCAGCATGATCCCGACGAGCAGAGCTTCCAA
ACGGTCT**TGA**ATTACAATGGACTTGACTCCACGCTTTCTAGAGATCAGGGTCTTTGGACTC
TTCTGCTCATTTGGAGCTCAAGTCAACAGCCACACAAACAGATGAGAGGTCACTTAAGTAGC
GTGAGCATTCGACGGGAACGATTCAATGAGCATTTTCTTATACAATACCAACAGCAAA
AGGATTGAAGCTGATTCACTGTAAAAAGGCATCTTATTGTGCTTTAGACCAAGTAGAAGG
AAAGCGAGGATCCAAATCTATTTTGTACACGAGGCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAACCTTTAATGTGGGATATTTTGATCAGTGCTTTGATTCACAAT
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACTATTGGATT
ATTAGTTATTCAAGCAGTCAAGCAGAACCCACAGGCTTATACACTCTACACATGTAT
TGAGCTAACCACTTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCAATAGGTTTGGGATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTATACATTAATCTCACTATTGTGATTAGGCCCAAAATAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGTTTCCATCTCTATGATGTT
ATGAGGATTGTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCAAAT
CAGATGCCCTCAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACAACTGTCAATT
TATCAACGTCCTTAGAAGAAATCTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAGAGTTA
CCCAACATACCATTTATGCTCTCTCTTCTGAGAAAACTGTAAACAGGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGTAGCCGGCA
TGGTGGCCAGGCACCTGTAGGAAATCCAGCAGGTGGAGGTGCACTGAGCCGAGATTATGCC
ATTGCACTCCAGCTGGTGCACAGAGCGGGAATCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLVSYVVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNIREDAEAPKARLVKPSSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCGAGCGAGAGCCGCTACCTGCAGCCGCGCCACGGCACGGCAGCCA
 CCAAGCGCCTCCTGCTGCTCTGCTCCTCTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAGAACGCCAAAGGGAAACTGCCATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CGAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGCTGGATCAAGTGATTATTTAT
 ATTCTGGAGACAAATTTTATGATGACTACTATCCAGATCTGAAGGCCGAGTACATTTTACCAGTAATGATCTC
 AAATCTGGTGATGCATCAATTAATGTAAAGCAATTTACAACCTGTCAGATATTGGCAGATATCAGTGCAAGGTGAA
 AAAAGCTCCTGGTGTTCGAATTAAGAAGATTCACTCGGTAGTCTTGTGTAAAGCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAAAGGTTCACATCCATTACAG
 TATGAGTGGCAAAATTTGCTGACTACAGAAAATGCCCACTTCATGGTTAGCAGAAATGACTTCATCTGTAT
 ATCTGTAAAAATGCCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAAACAGAGTGGGCTCTGATC
 AGTGCCCTGTTGGCTCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACATTAATGACAGGAGCCATATAGGAACT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGTAAAAAGCGCAGAGAAAGAAAATATGAAA
 GGAAGTTATCAGCATATCAGGAAGATGTGCCACTCCAAAGAGCCGTACGTCCACTGCCAGAGCTACATCG
 GCAGTAATCATTCATCCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAAGCGCACTCTCAGAGTCCGACTCTCCCACTGTGAAGTTCAAGTACCCCTTACAA
 GACTGATGGAATTAAGTTGATATAATATGGACTACTGAAGATCTGAAGTATTGTATTATTGACTTTATTTT
 AGGCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCAATGTCAAATTTAGTACGAGCCAAATTCCTGT
 TAAAAACCCCTATGTATAGTACACTGATAGTTAAAGATGTTTTTATTATATTTTCAATACTACCCTAACAA
 ATTTTTAACTTTTCATATGCATATTCGATATGTGGTCTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTACGTTCTGTTTAAATGTTTTTGCTATTAGTTAAATACATTGAAGGGAAATACCCG
 TTCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTCATGCCCTCAAATTTTTTTATTTGCAACTACA
 TGAATTTACACAATTTCTCTTAAACACAGCATAAATAGATTTCCCTGTATATAAATACTTACATACGCTCCA
 TAAAGTAAATCTCAAAGTCTAGAACAAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATTTAAAACTTAGGCATTTGACTAACTTTAATAAAATTTCTCAAACATA
 TATCAATATCTAAAGTGCATATATTTTAAAGAAAGATTATCTCAATAAGCTCTATAAAAAATAGTTTGTAGG
 TTTTCCGCCATCTAACTTCACTACTATTAGTAAGAACTTTTAACTTTAATGTGTAGTAGAGGTTTATTTCTACCTT
 TTTCTCAACATGCACCAACACAATCAAAAACGAAGTTAGTGAGGTCTAACATGTGAGGATTAAATCCAGTGAT
 TCCCGTCACAATGCATTCAGGAGGAGGTACCCATGTCACTGGAATTTGGCGGATATGGTTTATTTTTCTTCCC
 TGATTTGATACCAAAATGGAACAGGAGGATAGTGATTTCTGATGGCCATTCCCTCGATACATTTCTGGCTT
 TTTTCTGGGCAAGGCTGCCACATTTGAAGAGGTGGAATATAAGTTCTGAATCTGTAGGGAAGAGAACACAT
 TAAGTTAATTCAAAGGAAAAATCATCATATGTTCAGATTTCTCATTAAGACAAAGTTTACCACACACT
 GAGTCACATCTAAGTGACATCTCTATTGTCAAGCTCTAAATACATTAAAAACCTCATGTATAGGCGTATAA
 TGTATAACAGGTGACCAATGTTTTCTGAATCCATAAGAAATGAATAAATCAACAGTACTCTCTAAACAA
 CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTTGAAGGACATGCTTTTGTAGTCCAGTGGTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATCAACAACTGGAGCTGGAGGCCATTCTCTT
 AGCAAACTAATGCAGAAACAGAAATCAACTACCGCATGTTCTCACTTATAGTGGAGCTAATGATAAGACT
 TATGAACACAAGAGGAAACAAATAGACATTTGGAGTCTATTGAGAGGGGAGGGTGGGAGAACGAAAGAGCA
 GAAAGATAACTATTGAGTACGTCTTCAACCTGGGTGATGAAATAATATGTCACAACTCCCTCTGACACA
 TGTTTACCTATGGAAACAACTTCACTGTATCCCTAAACCTAAATAAAGTTAAAAAARAAAAA
 AAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA
 AAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSIITPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTCAGAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCTTCTGCCTCT
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCTGT
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCTGGCTGTGTCAGCAGGAGGTTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCT
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCGAAAATTTACAAAGC
 TCTGAATGCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTC
 AACAGTCTCCCTTCCATATGCTGTTCACCTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAACTCCTTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCTTGGTGCCTCTCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAAGACAACATAA
 CTCCAAAAA

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
```

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFCPPLLATASQMOMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK
 GVV PQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVTLLLEYFKLTVFKNH
 HNRTEVVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
 TKALGEVDILLTWMOKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCTATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCAGGTCCAACATGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGCCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTCCAACACCAGACGCTGGAACACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCTCTGTCCCGAGGAACGAGATCCCCCTAATCACTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCTCTGTTTCAGAGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGGGTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNsyHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRRGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTCTTCTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCAGCACCAGCCGAGAGCAGACTGCGATGACAACGGACGACACAGAAG
 TGCCCCGTATGACTTAGCACCAGGGCCAGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTACAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAGAGACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCTAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGACGATCAGAGAAATAGAAACAACAACCTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAAACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTGCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCAGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCAGGGGCCAGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGGTTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACCTTACCC
 CTTACAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCTT
 CTTCTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCAGACTGCCCGGAC
 GAGGCCGACCACAGCAG**TGA**GTGAGGTGAAAATGGAGGTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCCAGCCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGCTCTGGACTCACCTTGG
 CACATGTTCTGTGTTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
 TTAATAATTCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLPAGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVTQITGSDPEEAFDITLCTDDSSSEAKTLTMDILTALHTSTEAKGLSESSASSDGPHV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEFPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEALKNFPTSETPTMDIATKGFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGGGATTCGCCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCGAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACCTCAACTCAAGAAGACTGCAATTAATCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAAACCACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTTACATGGCCAAATTTTCACAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTTATAAGGAAAAAGGCCATTTCTCAGAGTTCACAAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCGTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCAGCACCTCATTTCTACAGTTTTTACAGGGCTCGGGCTACACTCCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTTAACTTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAACTCAGTACGGCCCTTC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGAGGAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAAGCCCAATGCAATGAGTTTCTGCTGACTGTAGTCTTAGCAGGAGGTTG
 TATTTTGAGACAGGAAAAATGCCCTTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAAGTACGACGATCTCGGCTCTCACCACAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCCACATGTTGGTCAGGCTG
 GTCTCAAACTCCTGACCTAGTGATCCACCTCTCGGCCCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTCTGTTTTATGTTTGGTTTTTGGAGGAATGAAGTG
 GGAACCAATTAGGTAATTTTGGTAATCTGCTCTAAATATTAGCTAAAAACAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAA
 GAAACAGGTTAGACATCTAGGTTCCAATTCATTCACTTCTTGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTTATATGGATTCTCTTAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTGTAATAATCTTTGTTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGEGSLTYTLVLIICFLTLRLSASQNCLKKSLLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTINTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCCA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTGCTGCTTCCAGGACCTCTATGCAGAAGAAAGGCCAGGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTACCCCTGCAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGCTTTCCAGGACCTGCTGTCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCTGACGGGAGCTCCCGCCCCCTATGCAGC
 TGGACTCCACTCAGCAGAGGACACCACTCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCGTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTCTGGCTCTCAGCCTTACTGCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGTGTCCCGGACTCCAGGGCTCTCCACACCTCCAGGCTCTCTCTTGCATGTCTCA
 GCCTGACCTTGAAGCGTTTGTACGCCCTGGAGCCACAGCGGCTGGCCTTGCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGCCCAGTGTGGACCTGCCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACGGTCTCTGCACTCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTCGGCCCAACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGAG
 GACTCTGAATTTAACAATGCCAGTGACTGTGCACTTGAAGTTGAGGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTACGCTTAGAGTCTGCATTTGGGCTGTGAGCTCTCCACTGGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCCAGGACCGGCACAGAAGTGG
 TTGCTTTNCCATTTGGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGCTCTCTTCTTGTCTGAAAGGGTTACTTGCTATGGGTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCAGTAGGTGTCTAACACAGAGAGATAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTGGAGAGGGGTGGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTCTTTTCCATTATATTGTTTTAAGACAGAACTCTCGTGT
 CTGCTCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCTCCGCTTCAAGTATT
 CTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTTTCAGTCTCCAAATTCGCCGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTCTCTTAAAAAGTGAATTAAGAGTTGTTCACTATGCAAACTTGGAAAG
 ATGGAAGAGAAAAAGAAAGGAAAGAAAAAATGTCAACCATAGTCTCAGCAGAGACTCAT
 TATTTTCGTTTTGTGTACTTCTTCCACTCTTTCTTCTTTCACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTTGTATATACACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGACTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELDRHKYWCRCGGILFSRCS
GTIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD E SLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG
TSQYGHERTSQYTGTSPPHATSPPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWSRLTAE EKEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128